



Full wwPDB EM Validation Report ⓘ

Apr 15, 2026 – 02:21 AM UTC

PDB ID : 9ZD7 / pdb_00009zd7
EMDB ID : EMD-74056
Title : The cryo-EM structure of Pakpunavirus P7-1 short tail fiber (gp92) bound to the extended baseplate
Authors : Li, F.; Cingolani, G.
Deposited on : 2025-11-25
Resolution : 4.20 Å(reported)

This is a Full wwPDB EM Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

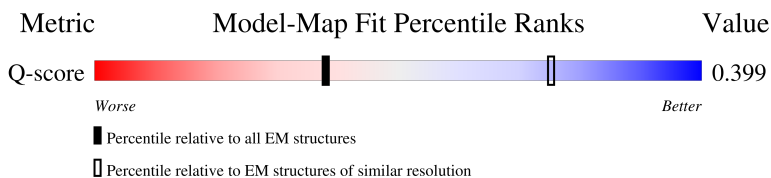
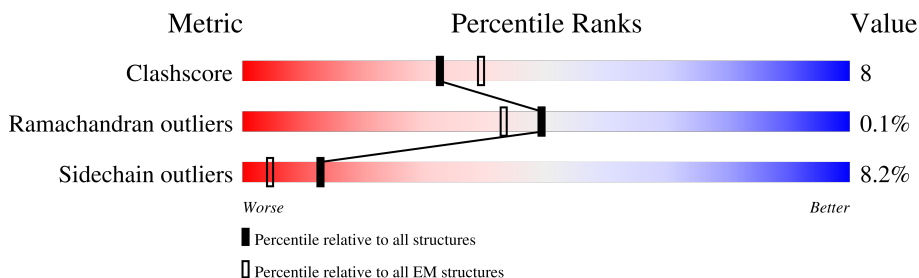
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 4.20 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	5410 (3.70 - 4.70)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	0	487	<div> <div>8%</div> <div>75%</div> <div>23%</div> <div>.</div> </div>
1	L	487	<div> <div>10%</div> <div>80%</div> <div>18%</div> <div>.</div> </div>
1	M	487	<div> <div>.</div> <div>75%</div> <div>22%</div> <div>.</div> </div>
1	N	487	<div> <div>.</div> <div>80%</div> <div>18%</div> <div>.</div> </div>



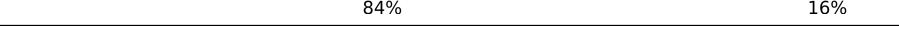
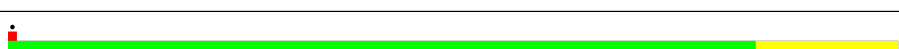



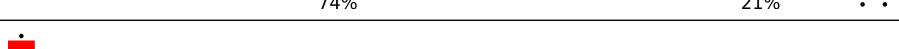



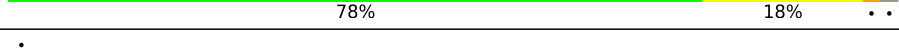

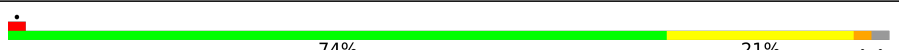


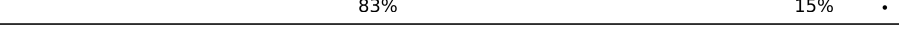







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Mol	Chain	Length	Quality of chain
1	V	487	
1	W	487	
1	X	487	
1	f	487	
1	g	487	
1	h	487	
1	o	487	
1	u	487	
2	l	243	
2	O	243	
2	Y	243	
2	i	243	
2	p	243	
2	v	243	
3	A	253	
3	B	253	
3	C	253	
3	D	253	
3	E	253	
3	F	253	
4	G	159	
4	Q	159	
4	a	159	
4	k	159	
4	q	159	

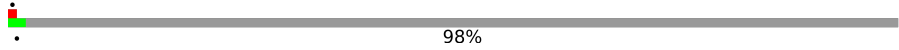
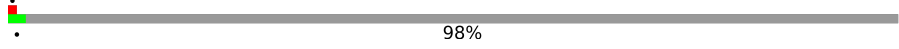
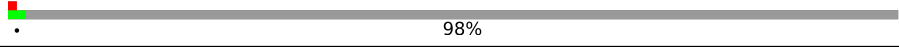
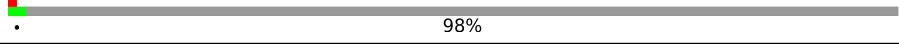
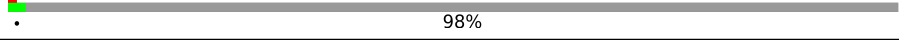
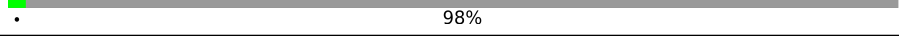
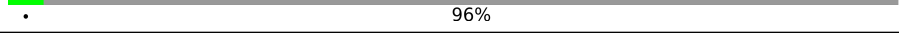
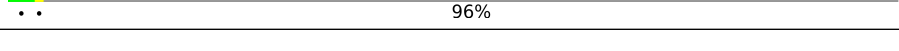
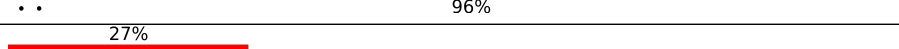
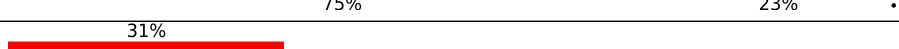
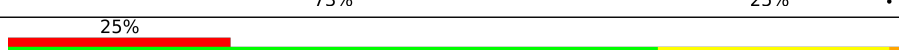

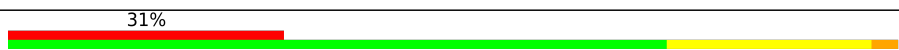

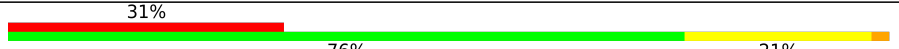





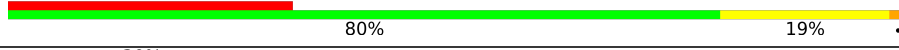
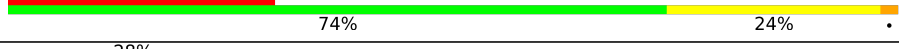



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Mol	Chain	Length	Quality of chain
4	w	159	
5	H	166	
5	R	166	
5	b	166	
5	l	166	
5	r	166	
5	x	166	
6	I	117	
6	S	117	
6	c	117	
6	m	117	
6	s	117	
6	y	117	
7	K	123	
7	U	123	
7	e	123	
7	n	123	
7	t	123	
7	z	123	
8	P	246	
8	Z	246	
8	j	246	
9	J	305	
9	T	305	
9	d	305	

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Mol	Chain	Length	Quality of chain
10	2	788	 98%
10	3	788	 98%
10	4	788	 98%
10	5	788	 98%
10	6	788	 98%
10	7	788	 98%
10	8	788	 96%
10	9	788	 96%
10	AA	788	 96%
11	AB	499	 27% 75% 23%
11	AC	499	 31% 73% 25%
11	AD	499	 25% 73% 26%
11	AE	499	 32% 74% 23%
11	AF	499	 31% 74% 23%
11	AG	499	 27% 77% 21%
11	AH	499	 31% 76% 21%
11	AI	499	 31% 74% 23%
11	AJ	499	 28% 75% 22%
11	AK	499	 29% 73% 25%
11	AL	499	 29% 76% 22%
11	AM	499	 25% 73% 24%
11	AN	499	 32% 80% 19%
11	AO	499	 30% 74% 24%
11	AP	499	 28% 78% 20%
11	AQ	499	 28% 78% 20%

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Mol	Chain	Length	Quality of chain
11	AR	499	<div><div></div><div>29%</div><div></div><div>74%</div><div></div><div>25%</div><div></div></div>
11	AS	499	<div><div></div><div>24%</div><div></div><div>76%</div><div></div><div>23%</div><div></div></div>

2 Entry composition [i](#)

There are 11 unique types of molecules in this entry. The entry contains 174969 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called gp88.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	0	486	Total 3681	C 2324	N 618	O 731	S 8	0	0
1	L	486	Total 3681	C 2324	N 618	O 731	S 8	0	0
1	M	486	Total 3681	C 2324	N 618	O 731	S 8	0	0
1	N	486	Total 3681	C 2324	N 618	O 731	S 8	0	0
1	V	486	Total 3681	C 2324	N 618	O 731	S 8	0	0
1	W	486	Total 3681	C 2324	N 618	O 731	S 8	0	0
1	X	486	Total 3681	C 2324	N 618	O 731	S 8	0	0
1	f	486	Total 3681	C 2324	N 618	O 731	S 8	0	0
1	g	486	Total 3681	C 2324	N 618	O 731	S 8	0	0
1	h	486	Total 3681	C 2324	N 618	O 731	S 8	0	0
1	o	486	Total 3681	C 2324	N 618	O 731	S 8	0	0
1	u	486	Total 3681	C 2324	N 618	O 731	S 8	0	0

- Molecule 2 is a protein called gp89.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	1	242	Total 1879	C 1201	N 315	O 362	S 1	0	0
2	O	242	Total 1879	C 1201	N 315	O 362	S 1	0	0
2	Y	242	Total 1879	C 1201	N 315	O 362	S 1	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
2	i	242	Total	C	N	O	S	0	0
			1879	1201	315	362	1		
2	p	242	Total	C	N	O	S	0	0
			1879	1201	315	362	1		
2	v	242	Total	C	N	O	S	0	0
			1879	1201	315	362	1		

- Molecule 3 is a protein called gp83.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	A	237	Total	C	N	O	S	0	0
			1876	1174	323	376	3		
3	B	237	Total	C	N	O	S	0	0
			1876	1174	323	376	3		
3	C	237	Total	C	N	O	S	0	0
			1876	1174	323	376	3		
3	D	237	Total	C	N	O	S	0	0
			1876	1174	323	376	3		
3	E	237	Total	C	N	O	S	0	0
			1876	1174	323	376	3		
3	F	237	Total	C	N	O	S	0	0
			1876	1174	323	376	3		

- Molecule 4 is a protein called gp79.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	G	158	Total	C	N	O	S	0	0
			1237	775	216	241	5		
4	Q	158	Total	C	N	O	S	0	0
			1237	775	216	241	5		
4	a	158	Total	C	N	O	S	0	0
			1237	775	216	241	5		
4	k	158	Total	C	N	O	S	0	0
			1237	775	216	241	5		
4	q	158	Total	C	N	O	S	0	0
			1237	775	216	241	5		
4	w	158	Total	C	N	O	S	0	0
			1237	775	216	241	5		

- Molecule 5 is a protein called gp78.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	H	166	Total	C	N	O	S	0	0
			1281	818	212	243	8		
5	R	166	Total	C	N	O	S	0	0
			1281	818	212	243	8		
5	b	166	Total	C	N	O	S	0	0
			1281	818	212	243	8		
5	l	166	Total	C	N	O	S	0	0
			1281	818	212	243	8		
5	r	166	Total	C	N	O	S	0	0
			1281	818	212	243	8		
5	x	166	Total	C	N	O	S	0	0
			1281	818	212	243	8		

- Molecule 6 is a protein called gp84.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	I	114	Total	C	N	O	S	0	0
			956	624	152	176	4		
6	S	114	Total	C	N	O	S	0	0
			956	624	152	176	4		
6	c	114	Total	C	N	O	S	0	0
			956	624	152	176	4		
6	m	114	Total	C	N	O	S	0	0
			956	624	152	176	4		
6	s	114	Total	C	N	O	S	0	0
			956	624	152	176	4		
6	y	114	Total	C	N	O	S	0	0
			956	624	152	176	4		

- Molecule 7 is a protein called gp87.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	K	120	Total	C	N	O	S	0	0
			979	628	163	183	5		
7	U	120	Total	C	N	O	S	0	0
			979	628	163	183	5		
7	e	120	Total	C	N	O	S	0	0
			979	628	163	183	5		
7	n	120	Total	C	N	O	S	0	0
			979	628	163	183	5		
7	t	120	Total	C	N	O	S	0	0
			979	628	163	183	5		
7	z	120	Total	C	N	O	S	0	0
			979	628	163	183	5		

- Molecule 8 is a protein called tail tip gp86.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	P	246	Total	C	N	O	S	0	0
			1874	1168	339	357	10		
8	Z	246	Total	C	N	O	S	0	0
			1874	1168	339	357	10		
8	j	246	Total	C	N	O	S	0	0
			1874	1168	339	357	10		

- Molecule 9 is a protein called gp85.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	J	304	Total	C	N	O	S	0	0
			2364	1463	415	475	11		
9	T	304	Total	C	N	O	S	0	0
			2364	1463	415	475	11		
9	d	304	Total	C	N	O	S	0	0
			2364	1463	415	475	11		

- Molecule 10 is a protein called gp88.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	4	19	Total	C	N	O		0	0
			143	85	27	31			
10	2	19	Total	C	N	O		0	0
			143	85	27	31			
10	3	19	Total	C	N	O		0	0
			143	85	27	31			
10	5	19	Total	C	N	O		0	0
			143	85	27	31			
10	6	19	Total	C	N	O		0	0
			143	85	27	31			
10	7	19	Total	C	N	O		0	0
			143	85	27	31			
10	8	32	Total	C	N	O	S	0	0
			255	152	45	57	1		
10	9	32	Total	C	N	O	S	0	0
			255	152	45	57	1		
10	AA	32	Total	C	N	O	S	0	0
			255	152	45	57	1		

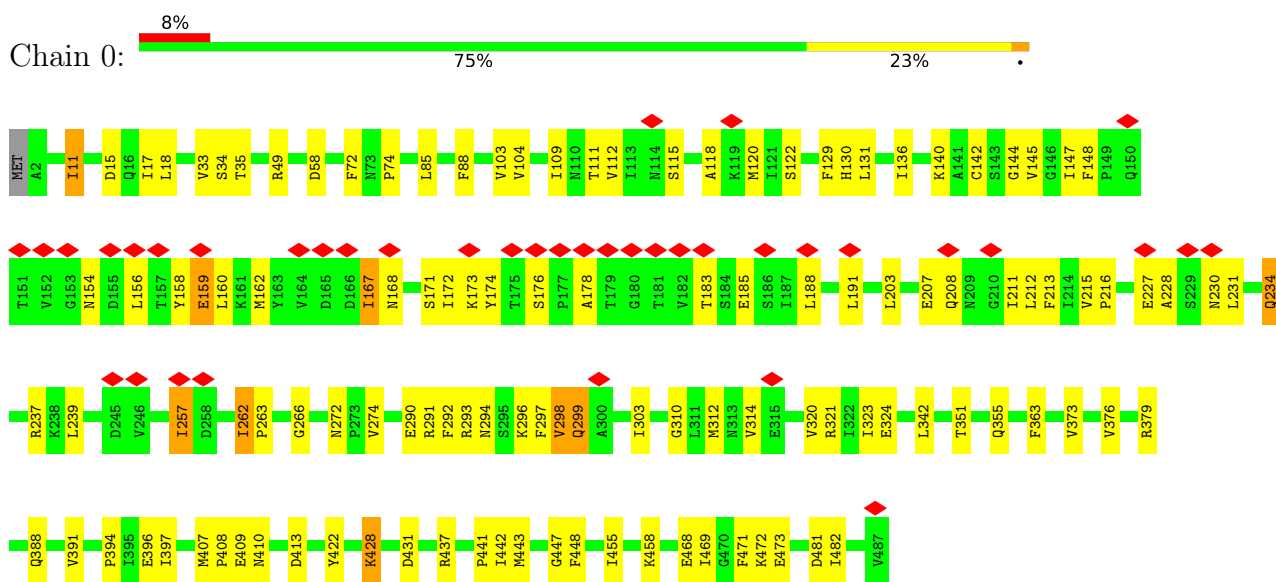
- Molecule 11 is a protein called short tail fiber gp92.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	AE	499	Total	C	N	O	S	0	0
			3734	2330	657	733	14		
11	AF	499	Total	C	N	O	S	0	0
			3734	2330	657	733	14		
11	AG	499	Total	C	N	O	S	0	0
			3734	2330	657	733	14		
11	AB	499	Total	C	N	O	S	0	0
			3734	2330	657	733	14		
11	AC	499	Total	C	N	O	S	0	0
			3734	2330	657	733	14		
11	AD	499	Total	C	N	O	S	0	0
			3734	2330	657	733	14		
11	AH	499	Total	C	N	O	S	0	0
			3734	2330	657	733	14		
11	AI	499	Total	C	N	O	S	0	0
			3734	2330	657	733	14		
11	AJ	499	Total	C	N	O	S	0	0
			3734	2330	657	733	14		
11	AK	499	Total	C	N	O	S	0	0
			3734	2330	657	733	14		
11	AL	499	Total	C	N	O	S	0	0
			3734	2330	657	733	14		
11	AM	499	Total	C	N	O	S	0	0
			3734	2330	657	733	14		
11	AN	499	Total	C	N	O	S	0	0
			3734	2330	657	733	14		
11	AO	499	Total	C	N	O	S	0	0
			3734	2330	657	733	14		
11	AP	499	Total	C	N	O	S	0	0
			3734	2330	657	733	14		
11	AQ	499	Total	C	N	O	S	0	0
			3734	2330	657	733	14		
11	AR	499	Total	C	N	O	S	0	0
			3734	2330	657	733	14		
11	AS	499	Total	C	N	O	S	0	0
			3734	2330	657	733	14		

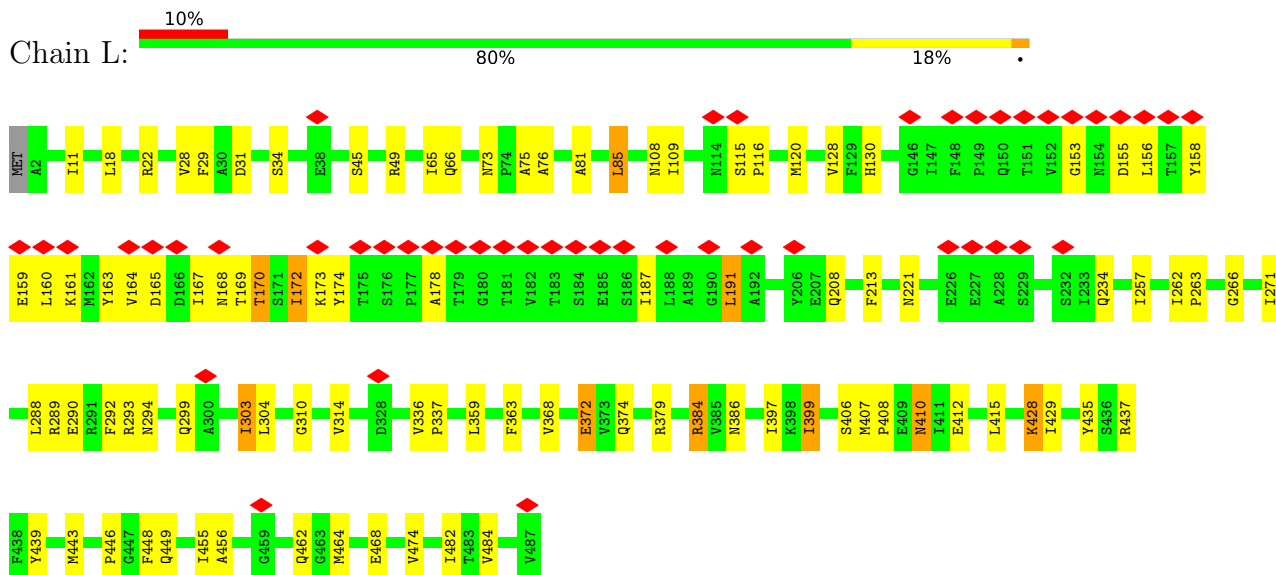
3 Residue-property plots

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.


• Molecule 1: gp88

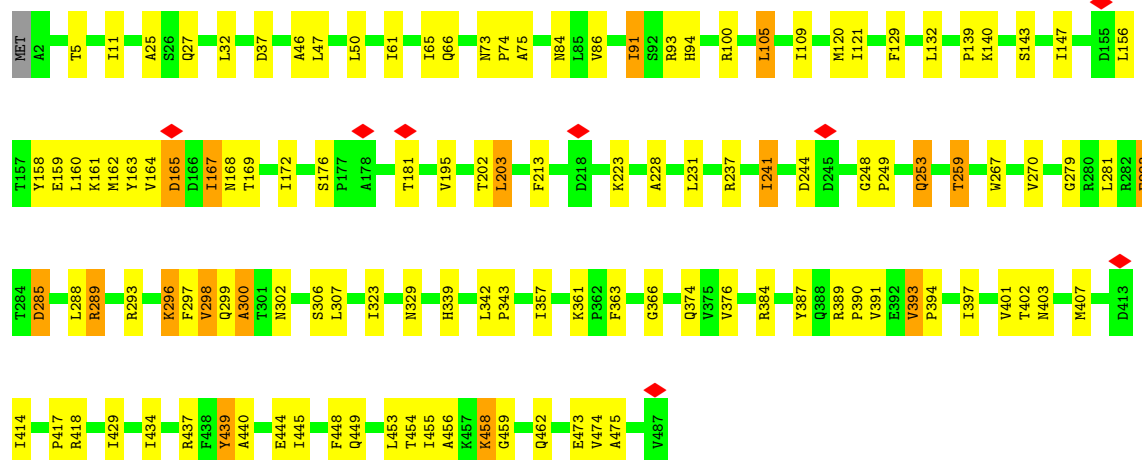


• Molecule 1: gp88




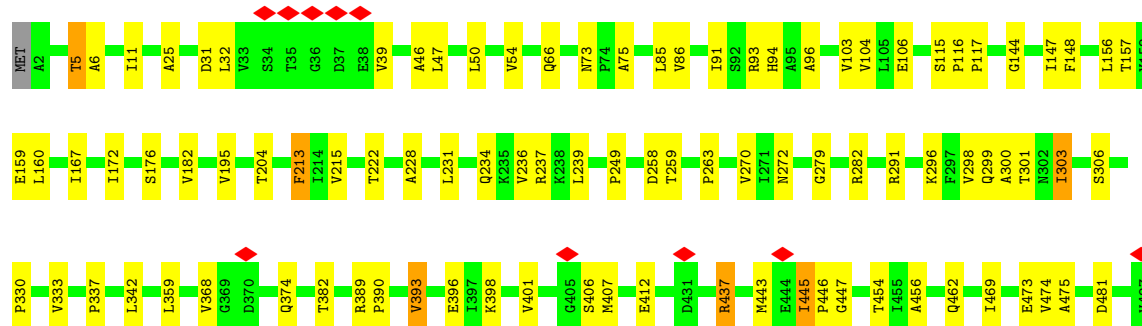
• Molecule 1: gp88

Chain M:  75% 22%




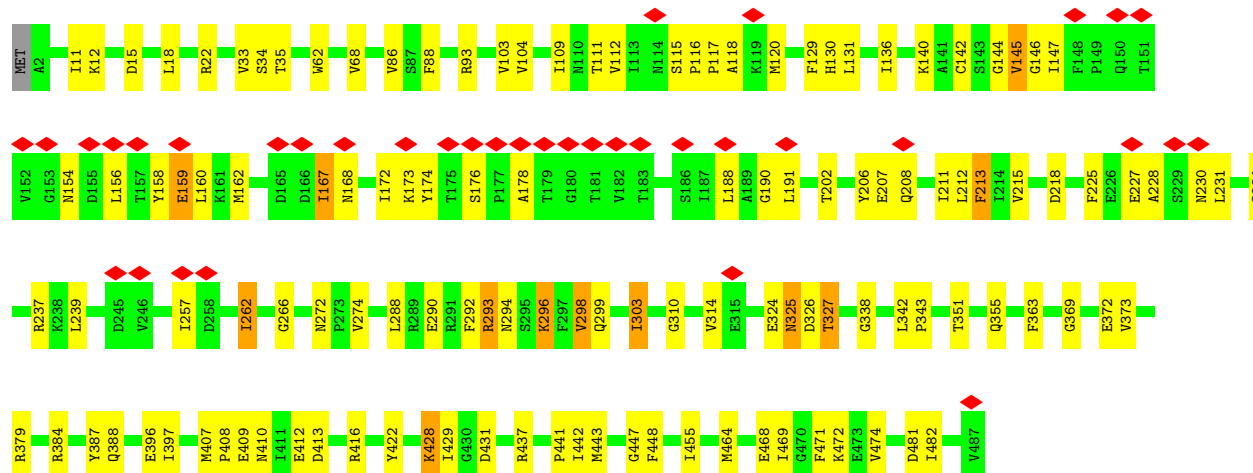
• Molecule 1: gp88

Chain N:  80% 18%




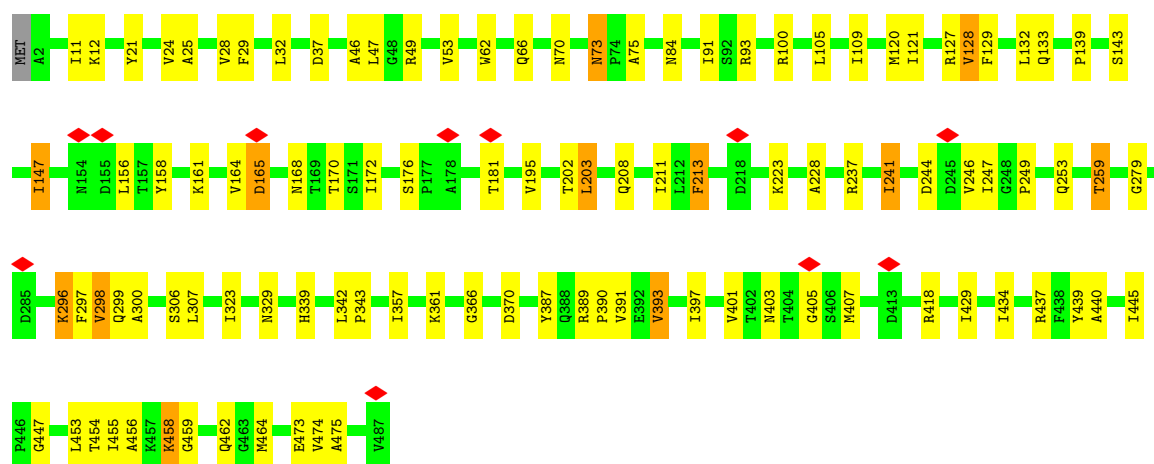
• Molecule 1: gp88

Chain V:  8% 74% 24%




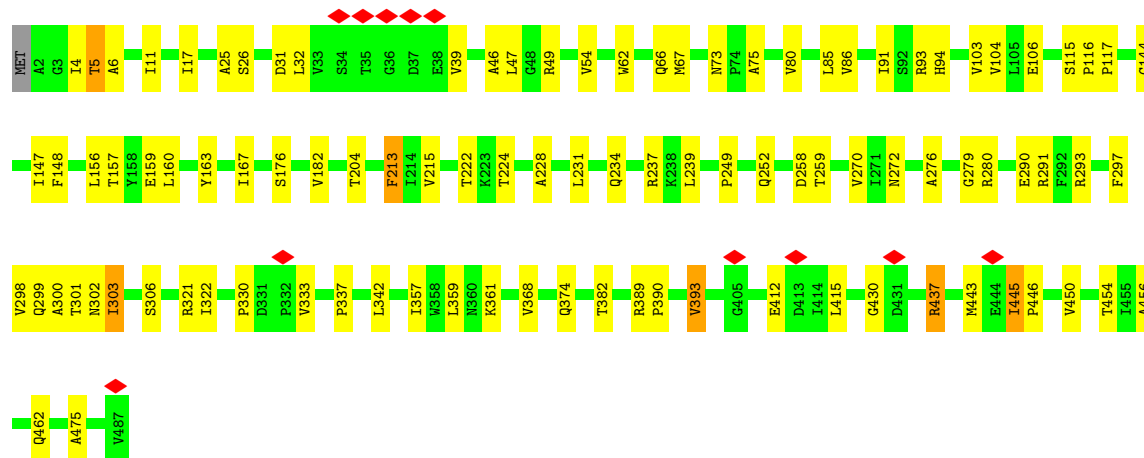
• Molecule 1: gp88

Chain W:  78% 19%




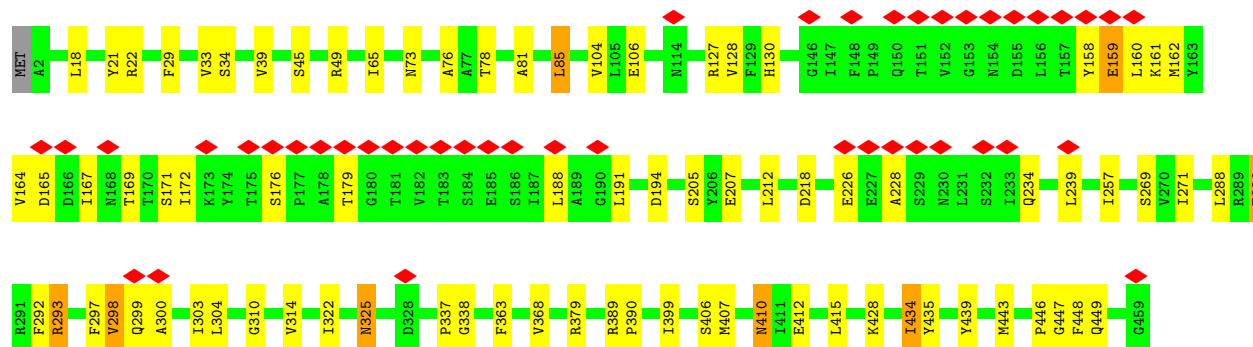
• Molecule 1: gp88

Chain X:  79% 19%



• Molecule 1: gp88

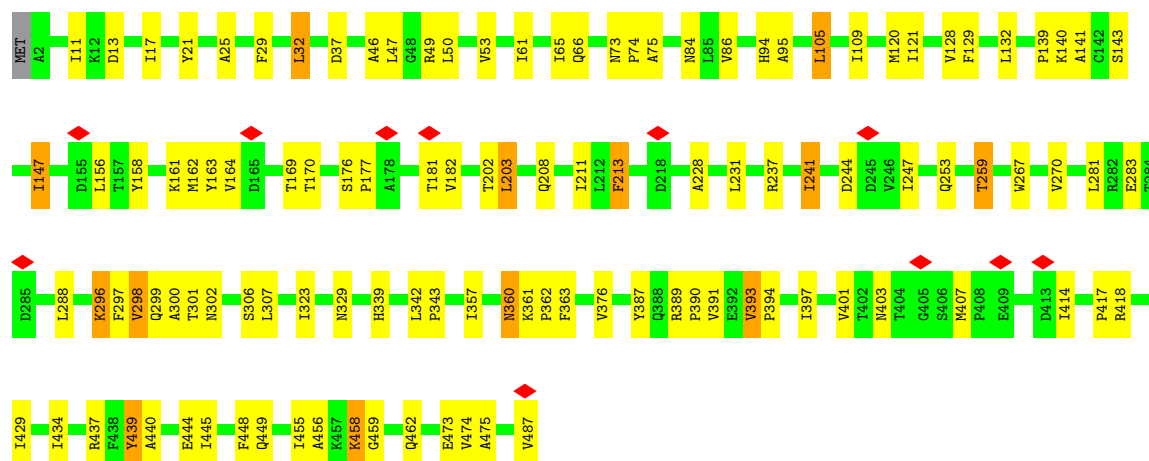
Chain f:  9% 82% 16%





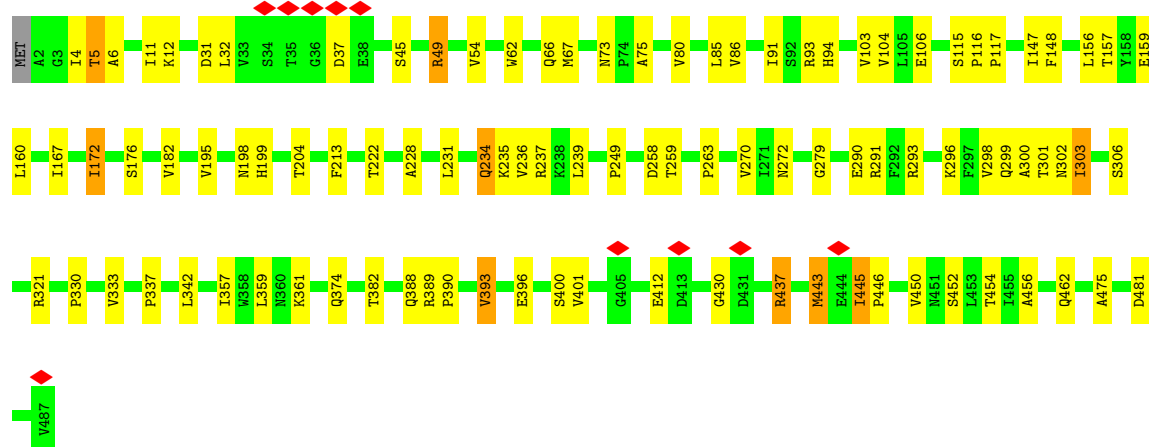
• Molecule 1: gp88

Chain g: 76% 21%



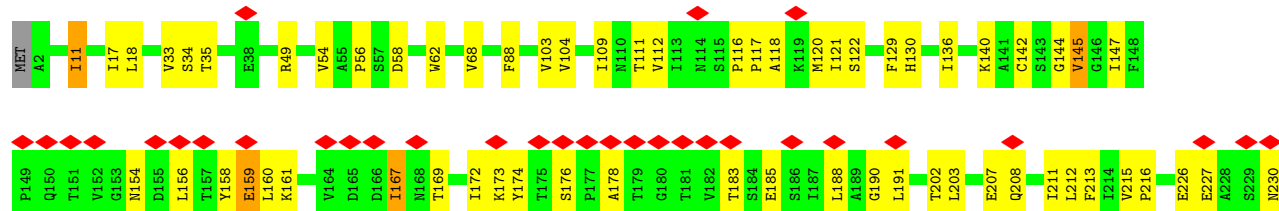
• Molecule 1: gp88

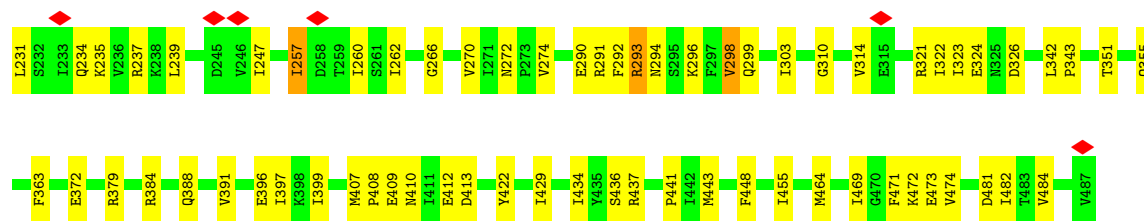
Chain h: 79% 18%



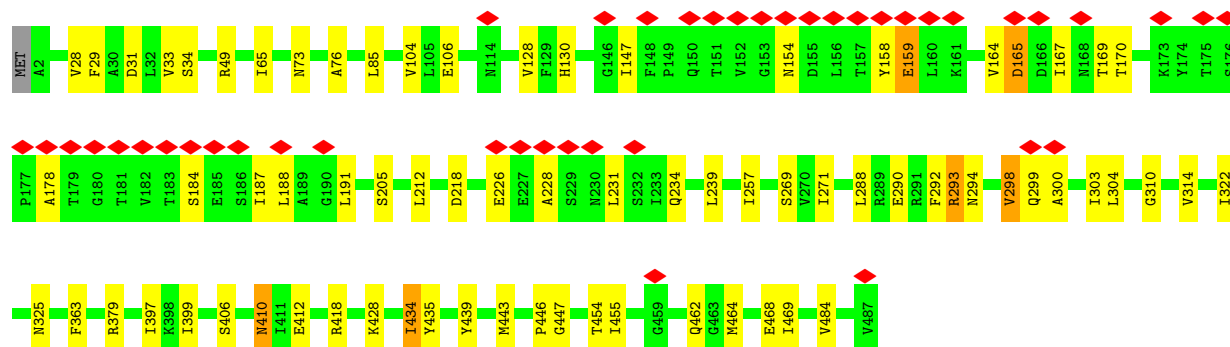
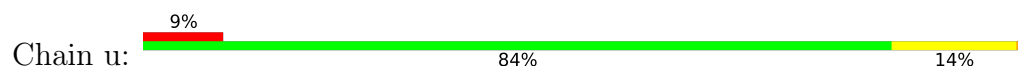
• Molecule 1: gp88

Chain o: 8% 74% 25%

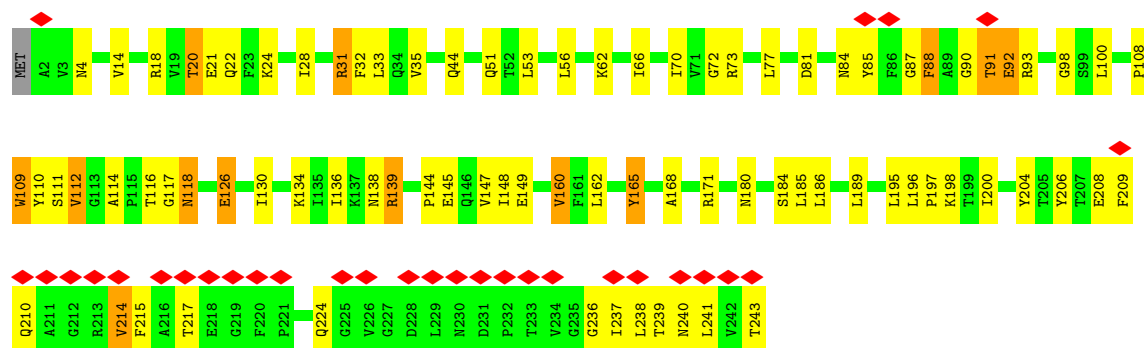




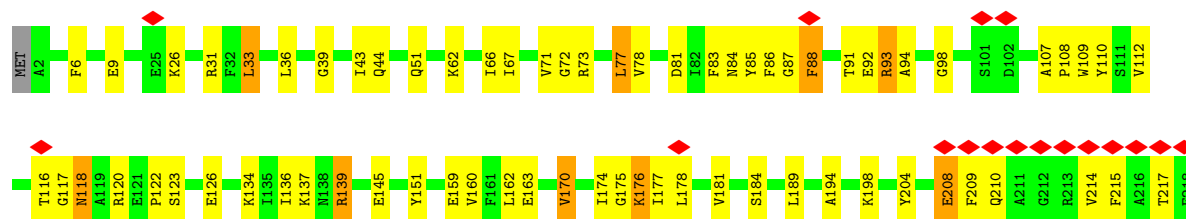
• Molecule 1: gp88

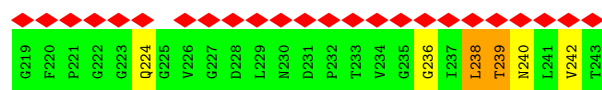


• Molecule 2: gp89

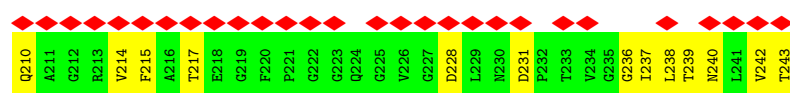
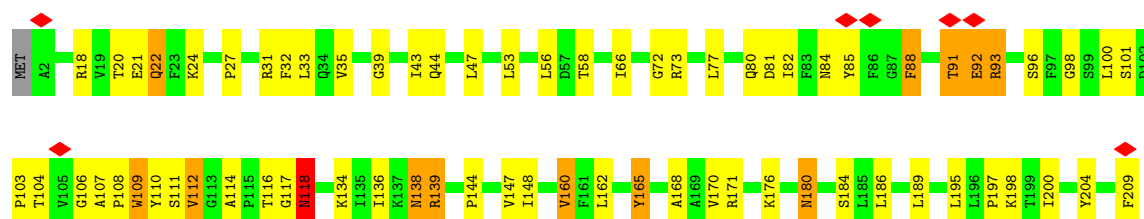


• Molecule 2: gp89

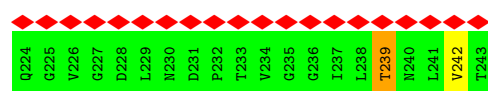
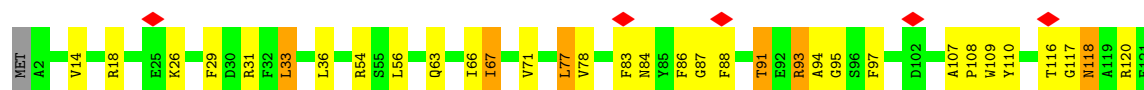




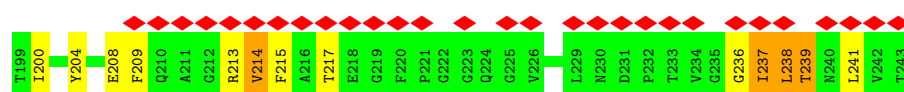
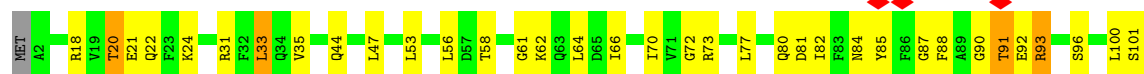
• Molecule 2: gp89



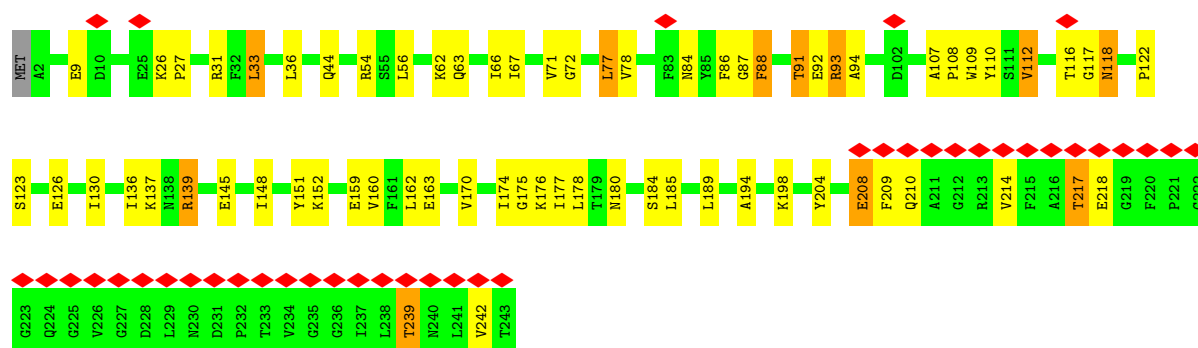
• Molecule 2: gp89



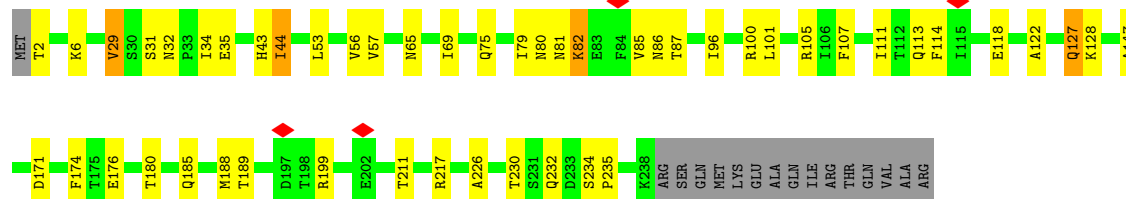
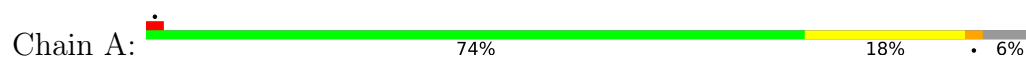
• Molecule 2: gp89



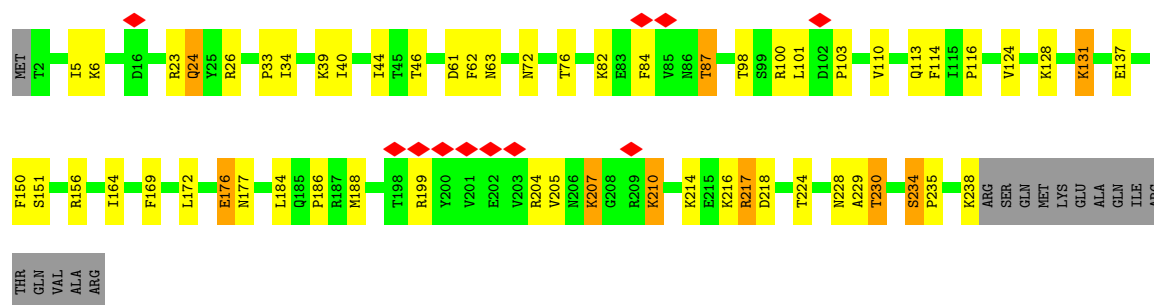
• Molecule 2: gp89



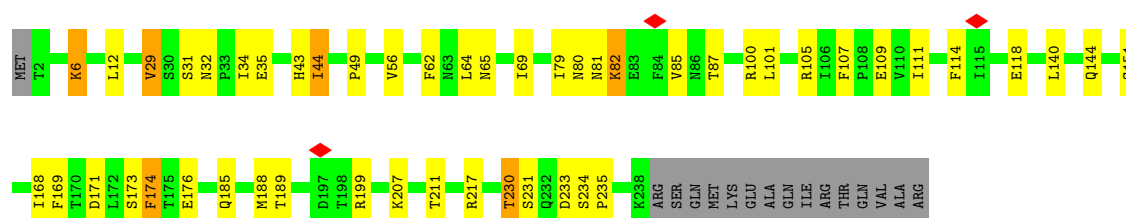
• Molecule 3: gp83



• Molecule 3: gp83

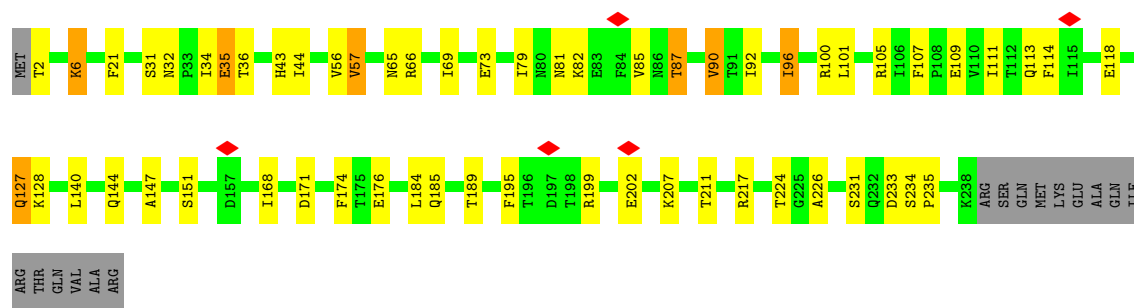


• Molecule 3: gp83



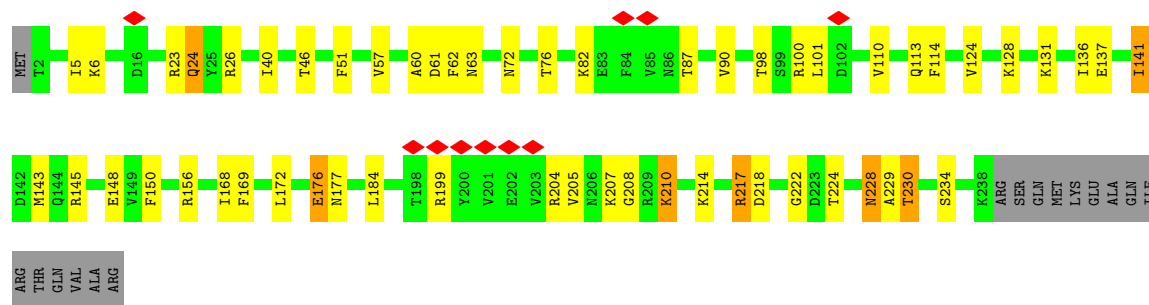
• Molecule 3: gp83

Chain D: 



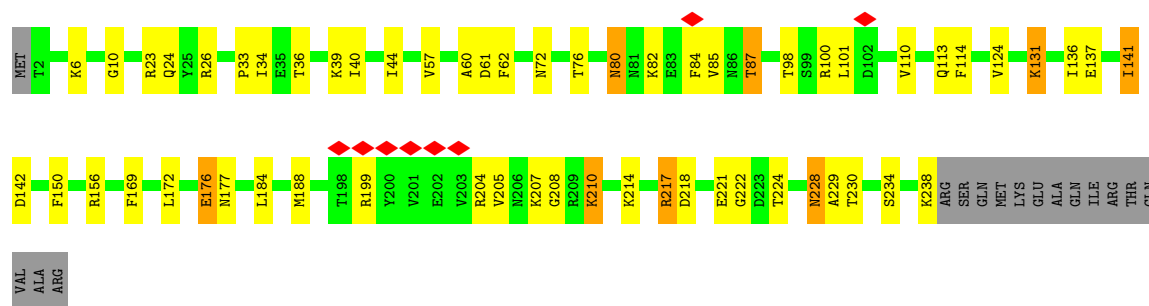
• Molecule 3: gp83

Chain E: 




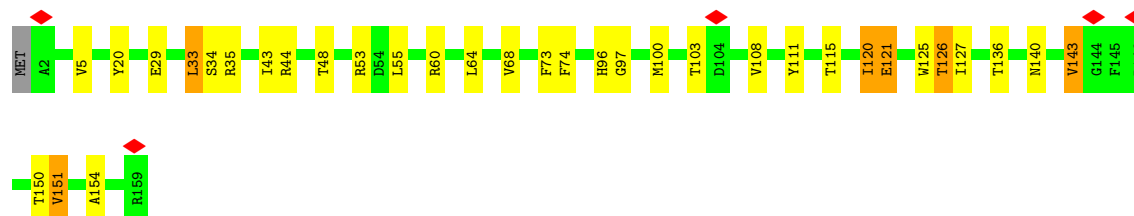
• Molecule 3: gp83

Chain F: 

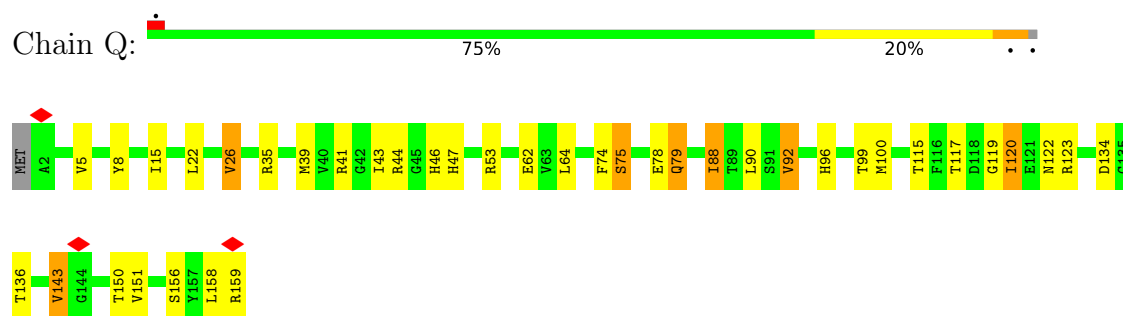


• Molecule 4: gp79

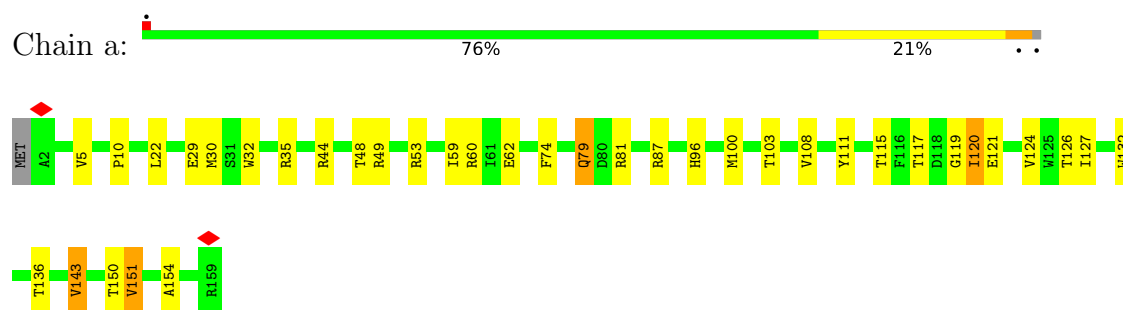
Chain G: 



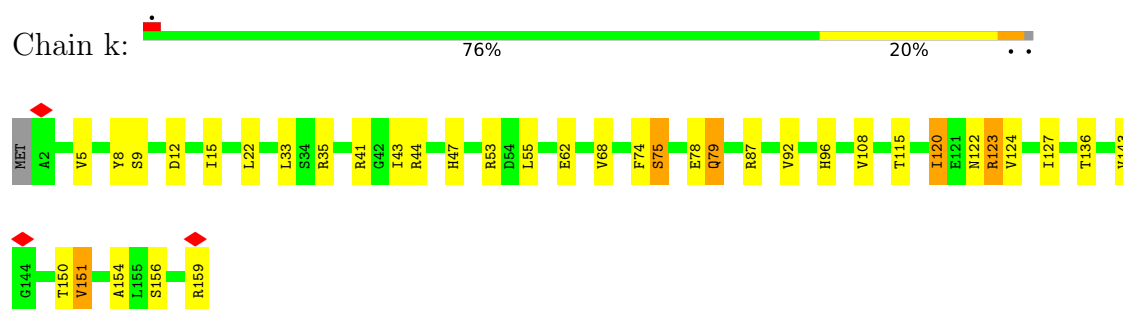
- Molecule 4: gp79



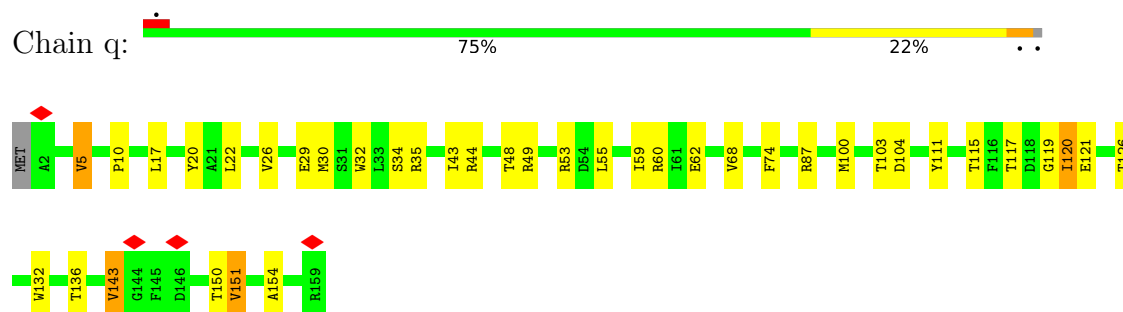
- Molecule 4: gp79



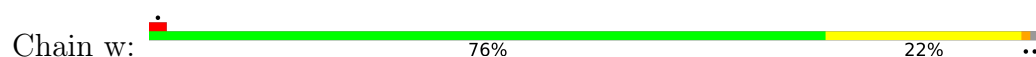
- Molecule 4: gp79



- Molecule 4: gp79



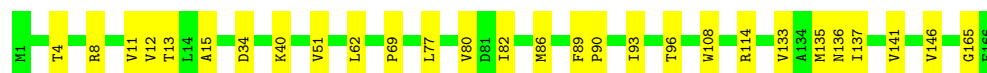
- Molecule 4: gp79





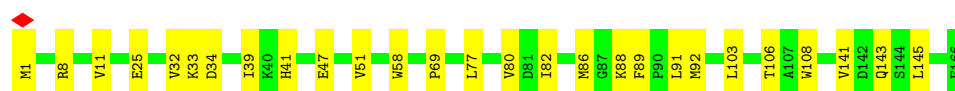
- Molecule 5: gp78

Chain H: 83% 17%



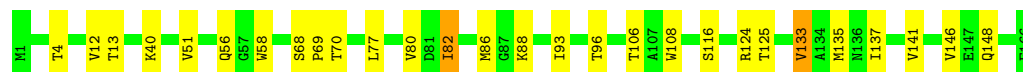
- Molecule 5: gp78

Chain R: 84% 16%



- Molecule 5: gp78

Chain b: 83% 16%



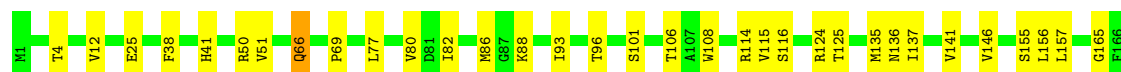
- Molecule 5: gp78

Chain l: 84% 16%



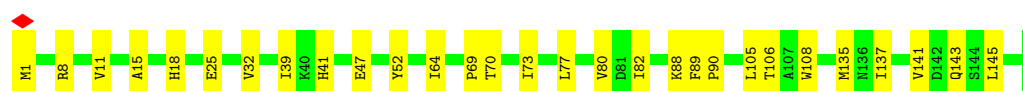
- Molecule 5: gp78

Chain r: 80% 19%




- Molecule 5: gp78

Chain x: 83% 17%



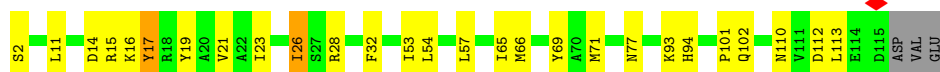
- Molecule 6: gp84

Chain I:  75% 21% ..



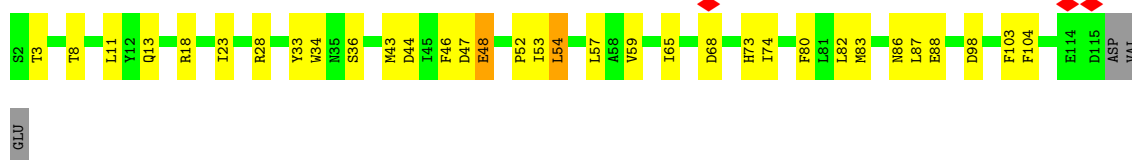
- Molecule 6: gp84

Chain S:  74% 21% ..




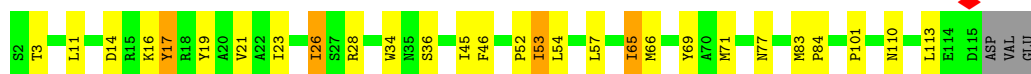
- Molecule 6: gp84

Chain c:  69% 26% ..



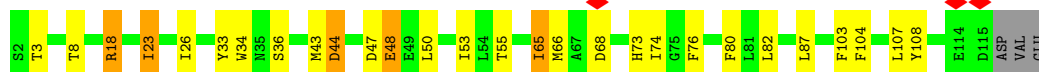
- Molecule 6: gp84

Chain m:  74% 21% ..



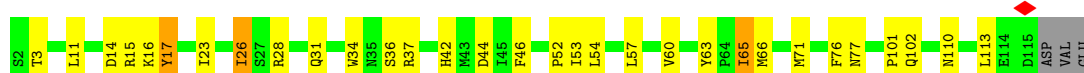
- Molecule 6: gp84

Chain s:  74% 20% ..




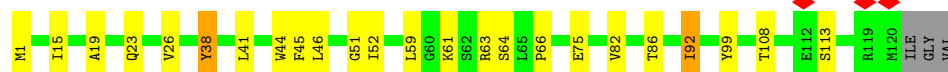
- Molecule 6: gp84

Chain y:  71% 24% ..




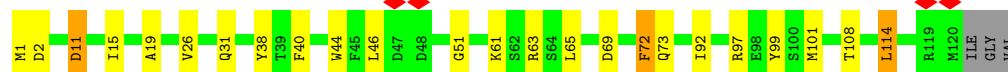
- Molecule 7: gp87

Chain K:  78% 18% ..




• Molecule 7: gp87

Chain U:  78% 17% ..



• Molecule 7: gp87

Chain e:  79% 16% ..



• Molecule 7: gp87

Chain n:  74% 21% ..




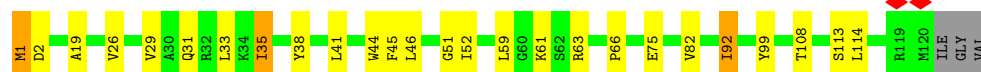
• Molecule 7: gp87

Chain t:  76% 20% ..




• Molecule 7: gp87

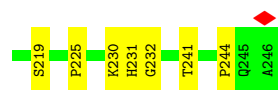
Chain z:  76% 19% ..



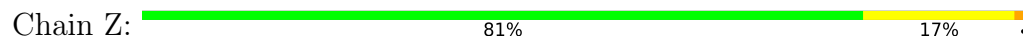
• Molecule 8: tail tip gp86

Chain P:  83% 15% .





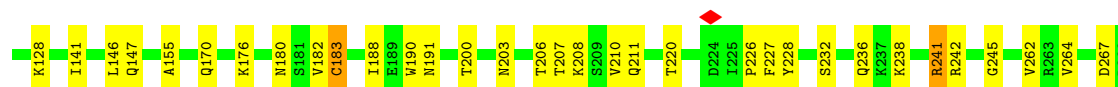
- Molecule 8: tail tip gp86



- Molecule 8: tail tip gp86

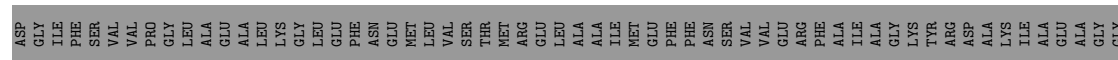


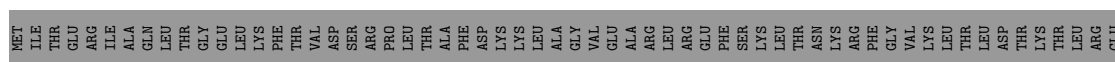
- Molecule 9: gp85



- Molecule 9: gp85



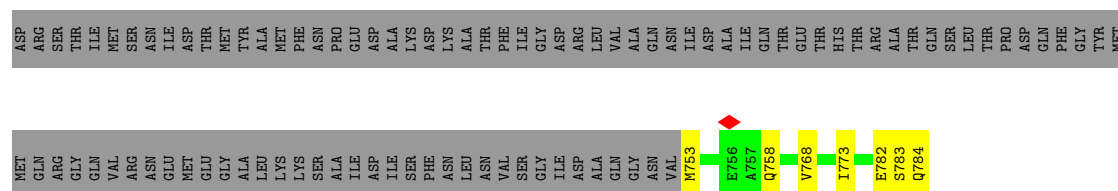








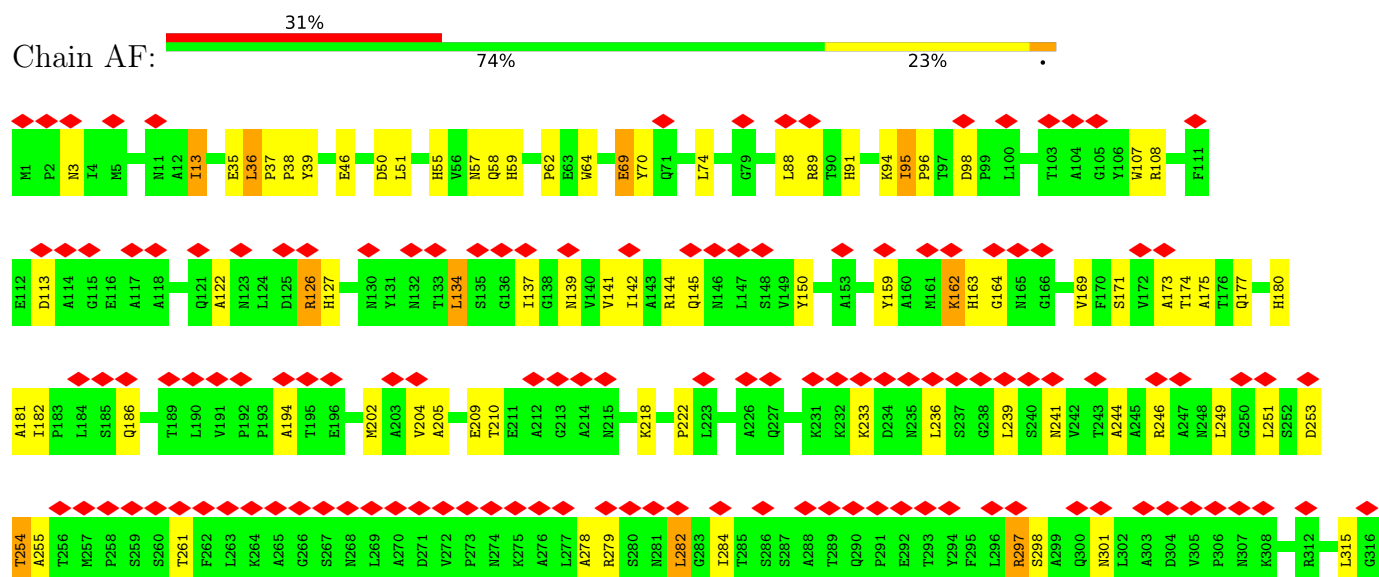
[illegible]

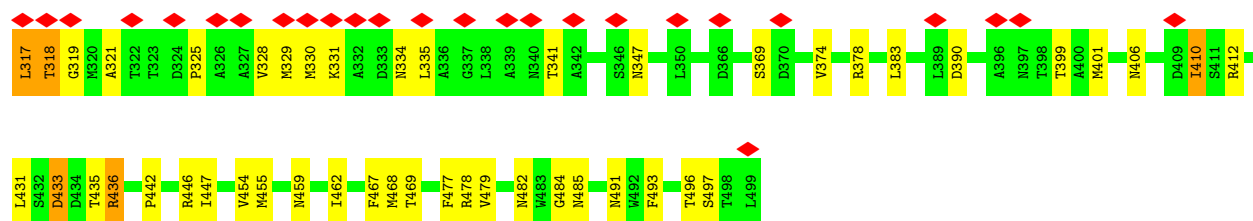


• Molecule 11: short tail fiber gp92

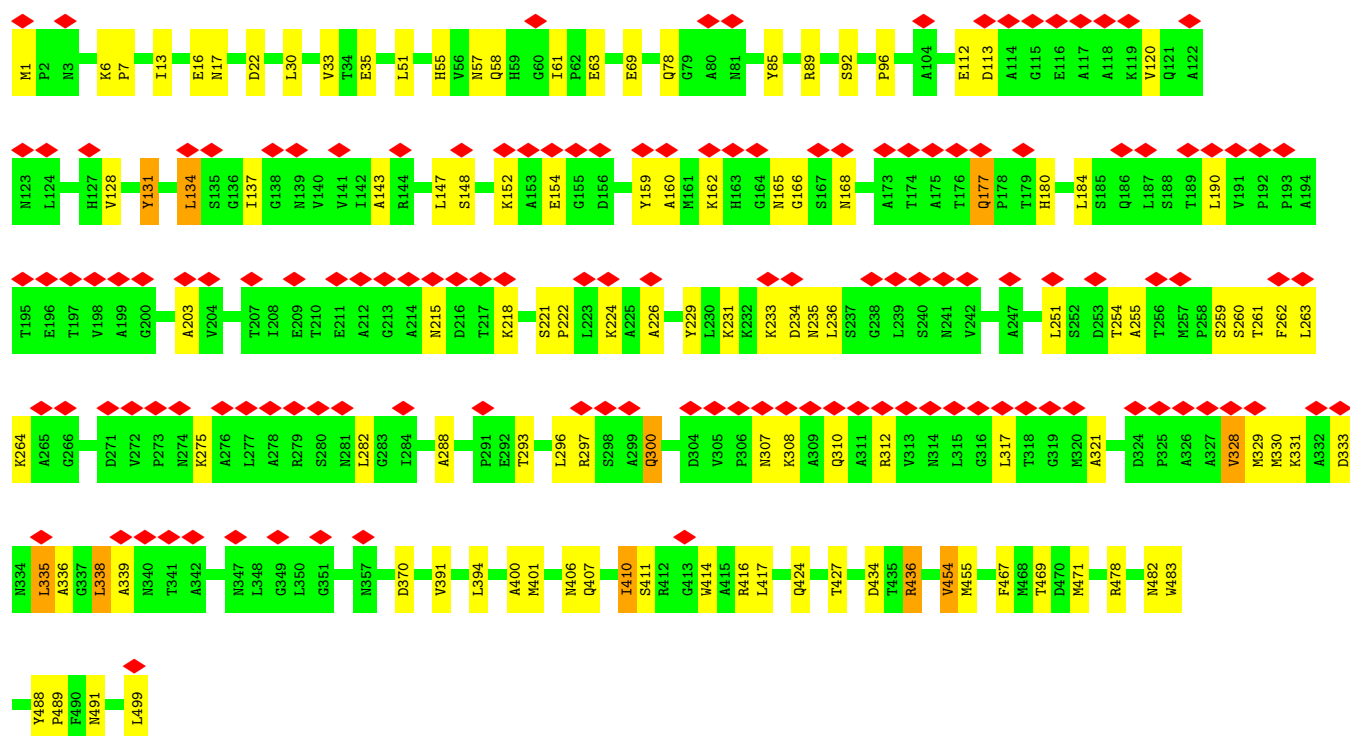
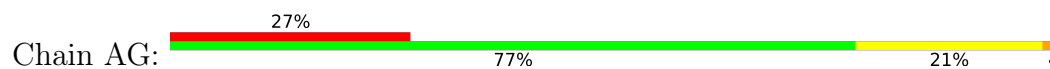


• Molecule 11: short tail fiber gp92

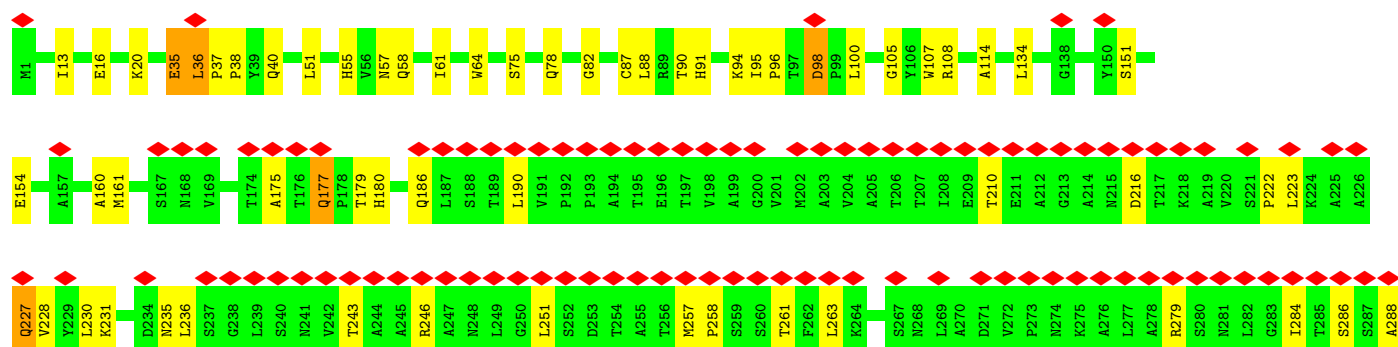
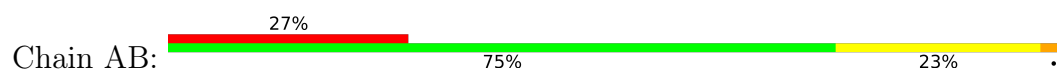


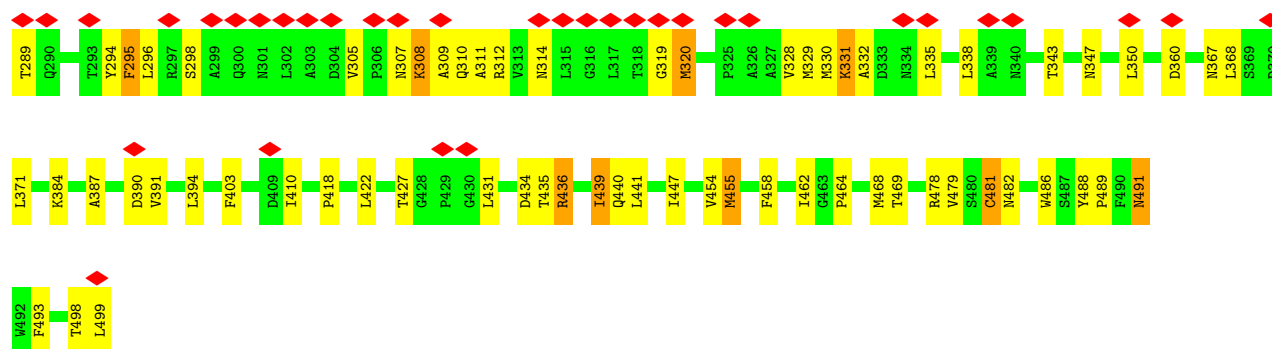


- Molecule 11: short tail fiber gp92

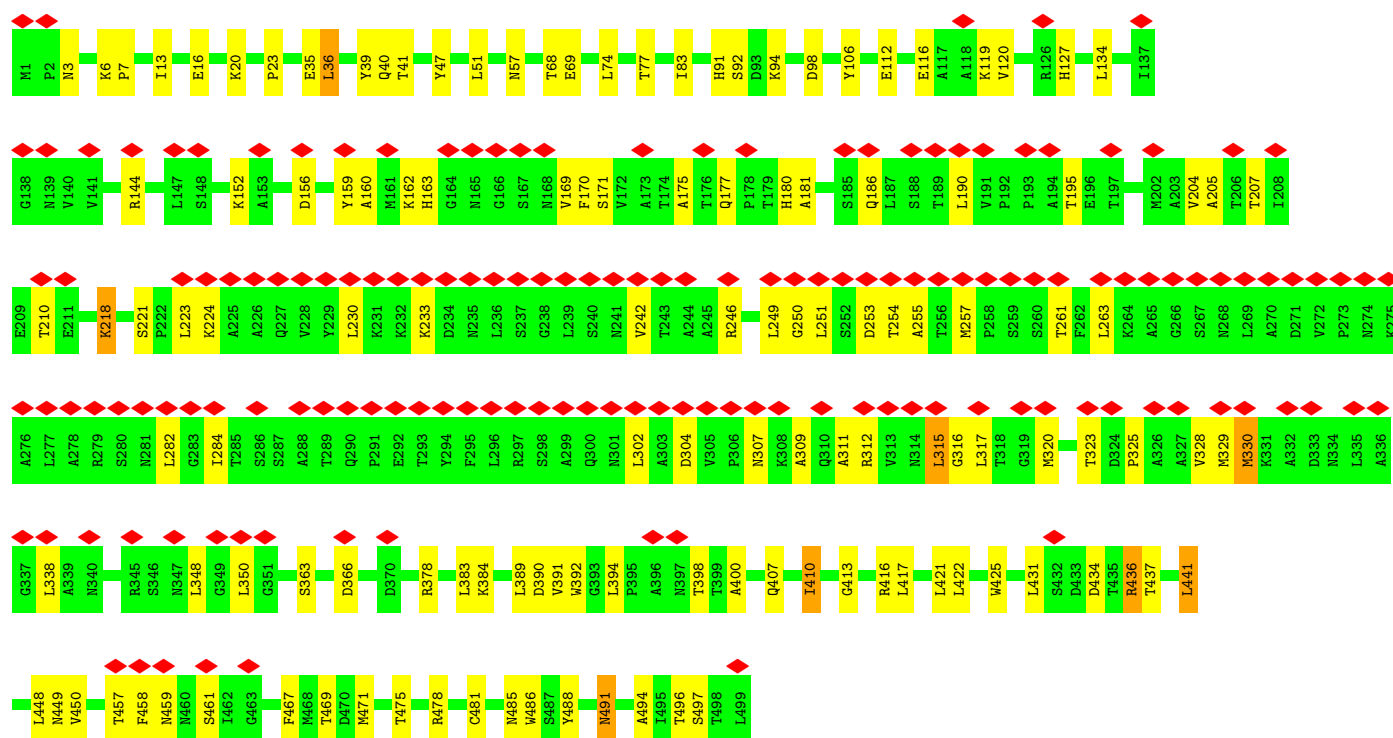
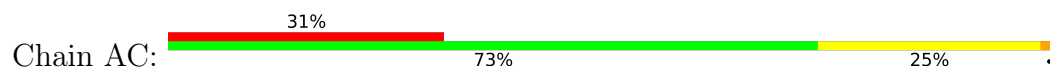


- Molecule 11: short tail fiber gp92

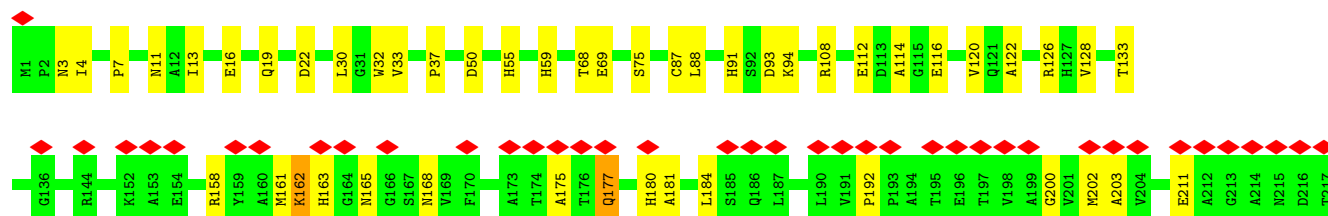
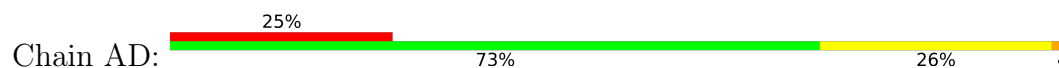




- Molecule 11: short tail fiber gp92

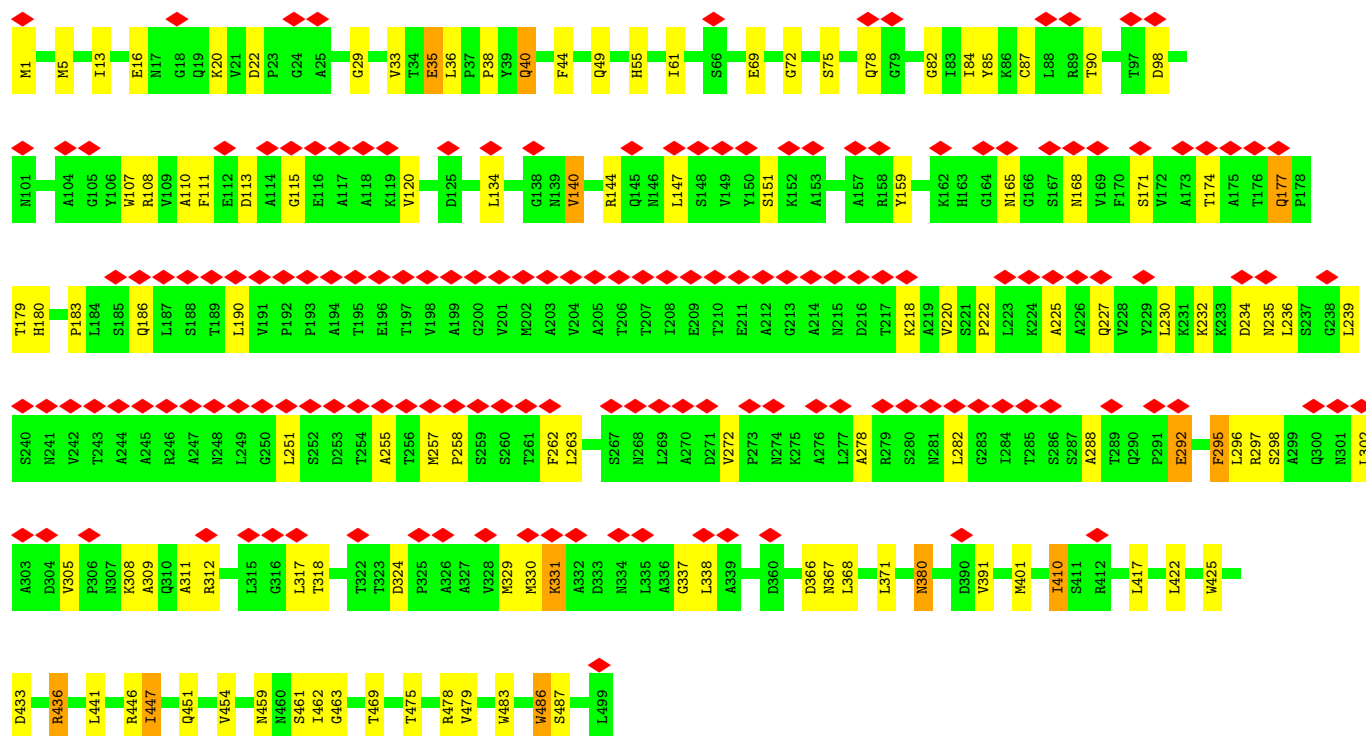
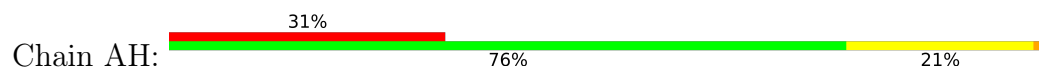


- Molecule 11: short tail fiber gp92

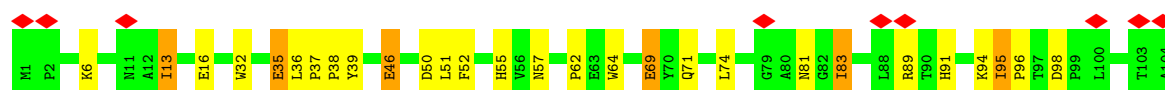
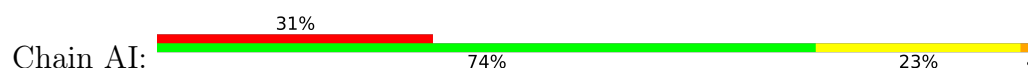


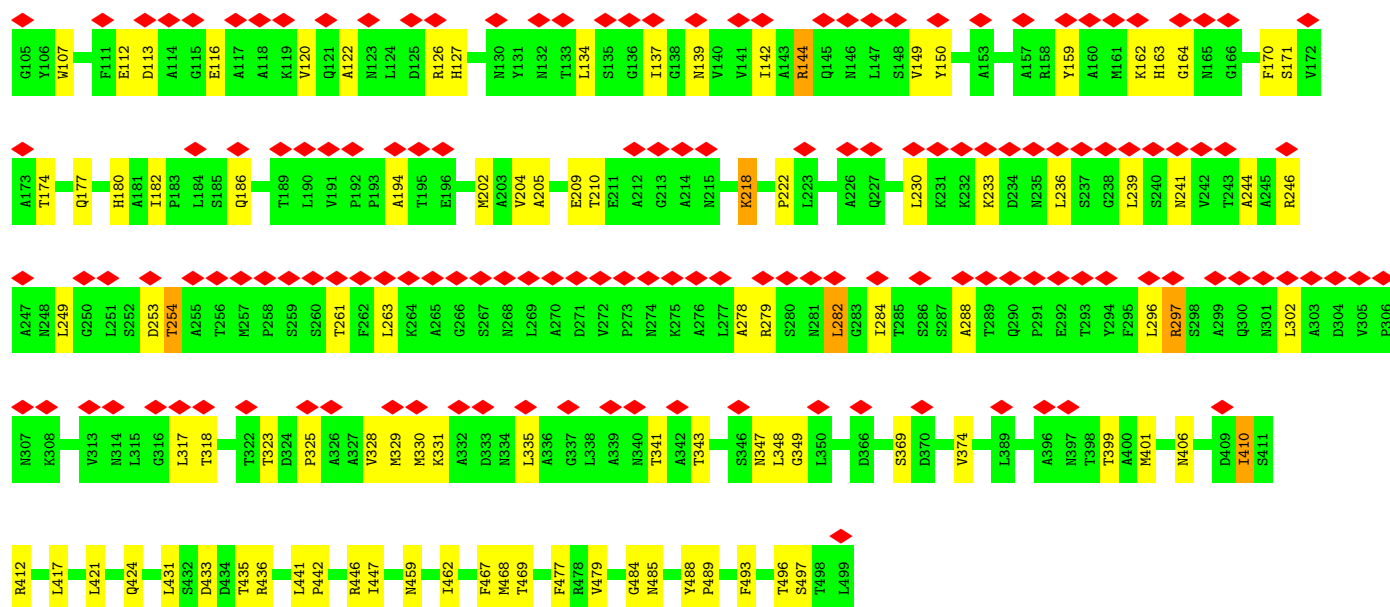


- Molecule 11: short tail fiber gp92

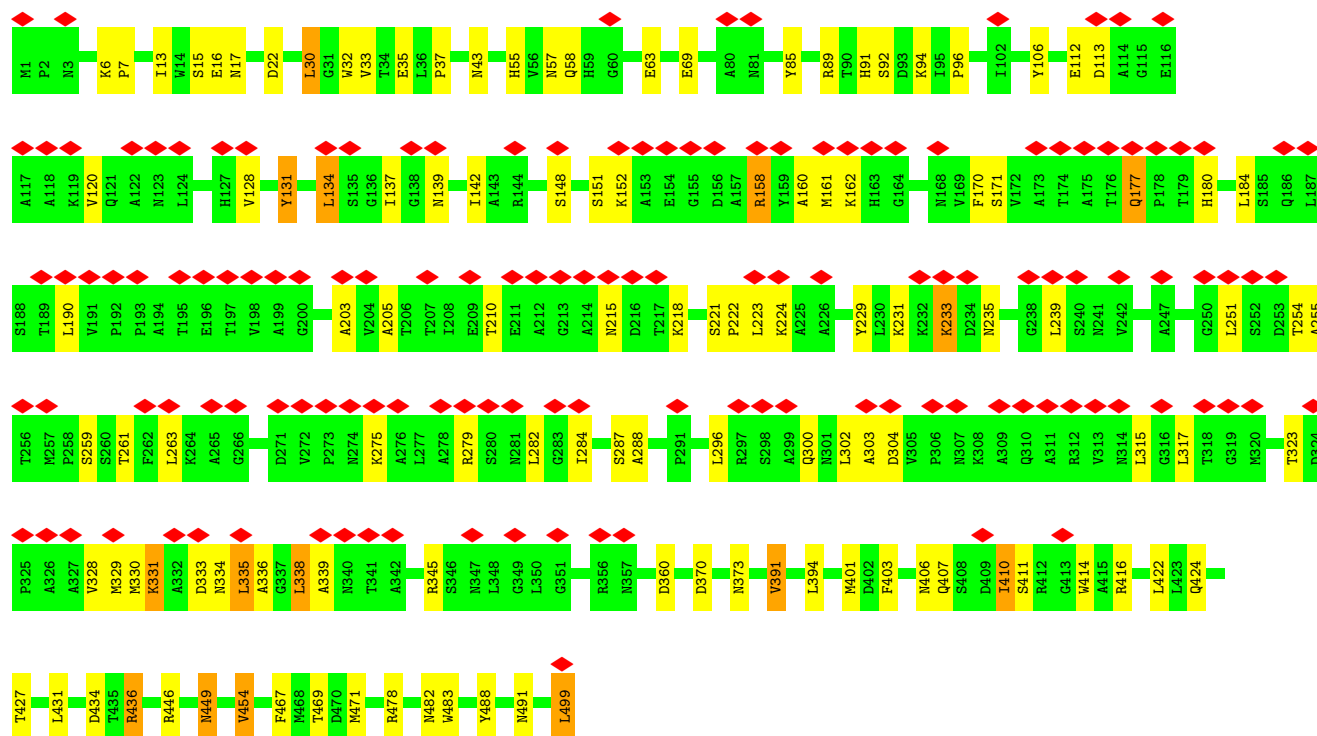
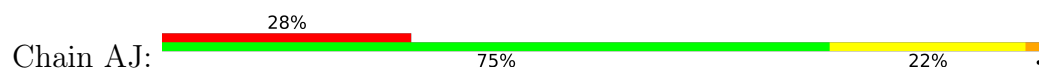


- Molecule 11: short tail fiber gp92

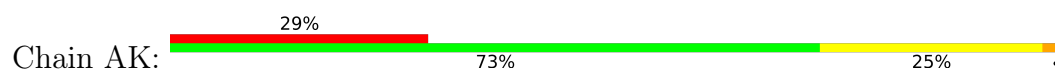


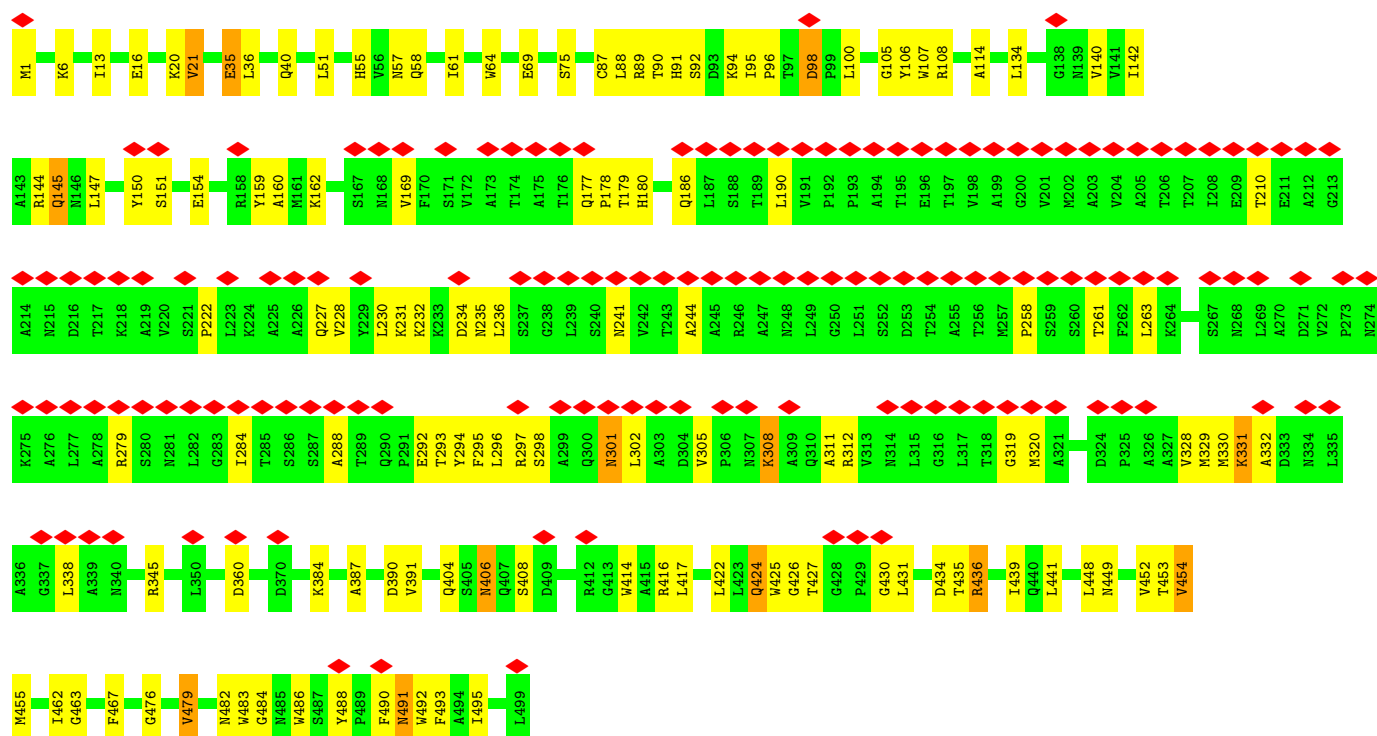


• Molecule 11: short tail fiber gp92

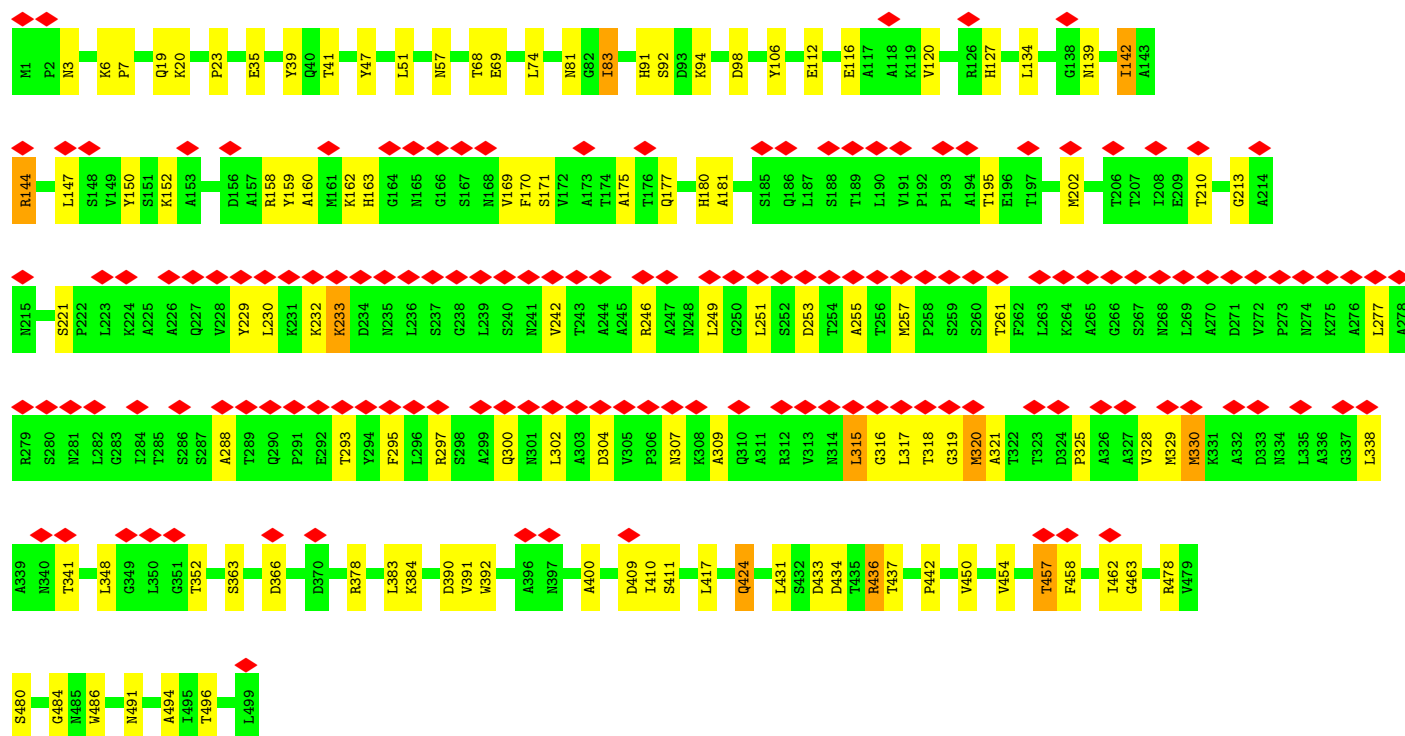
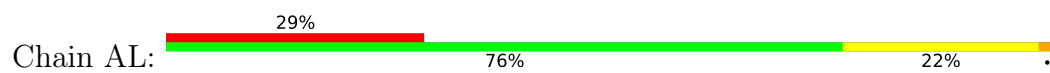


• Molecule 11: short tail fiber gp92

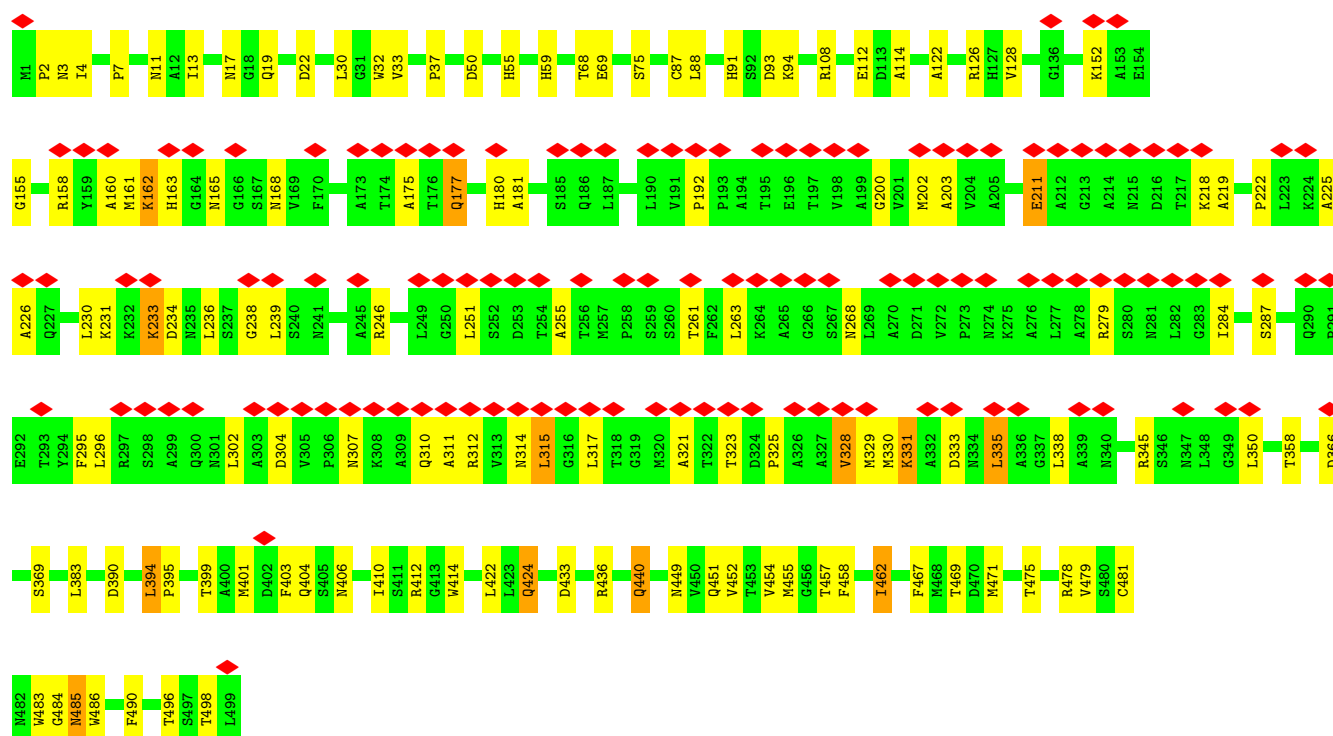
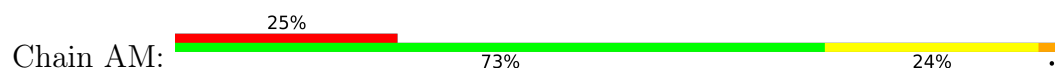




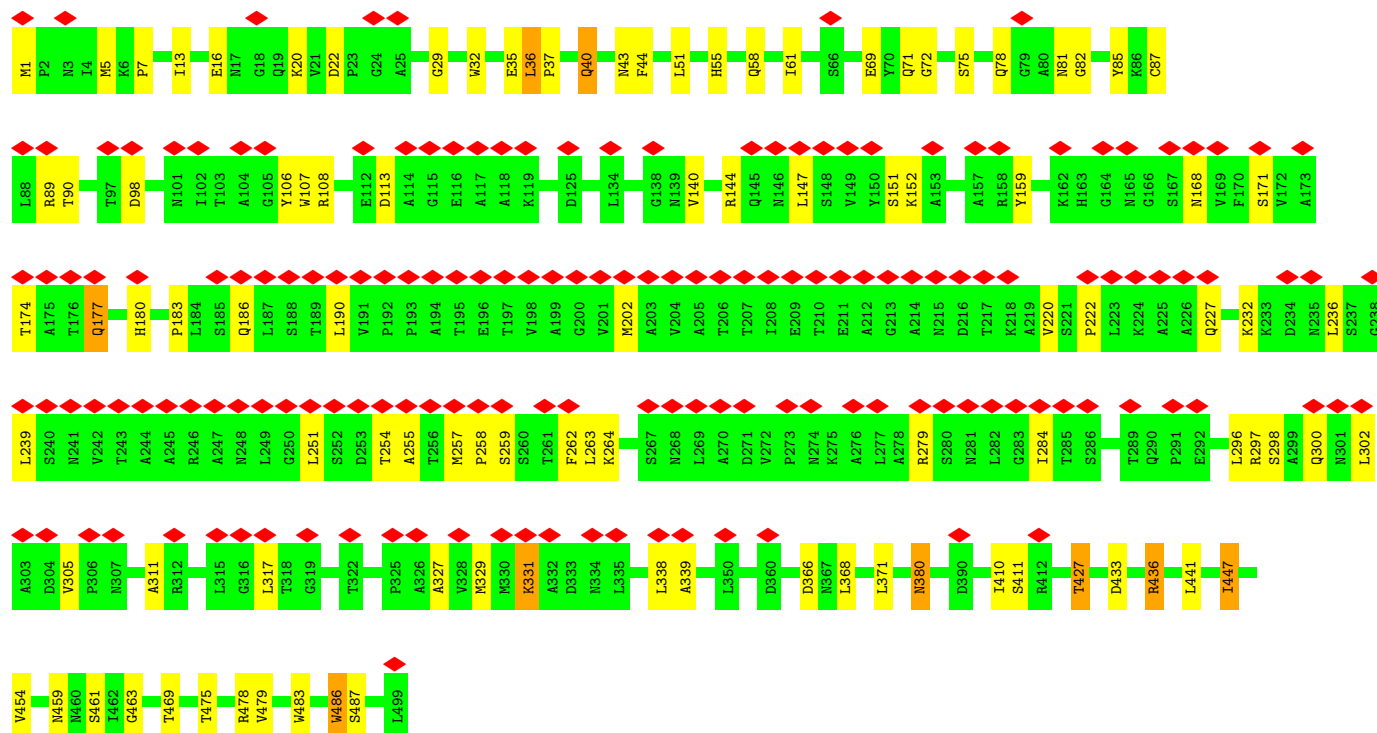
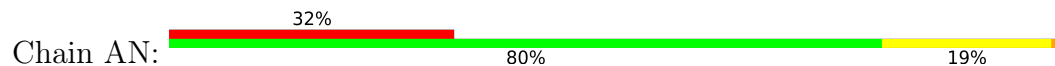
• Molecule 11: short tail fiber gp92



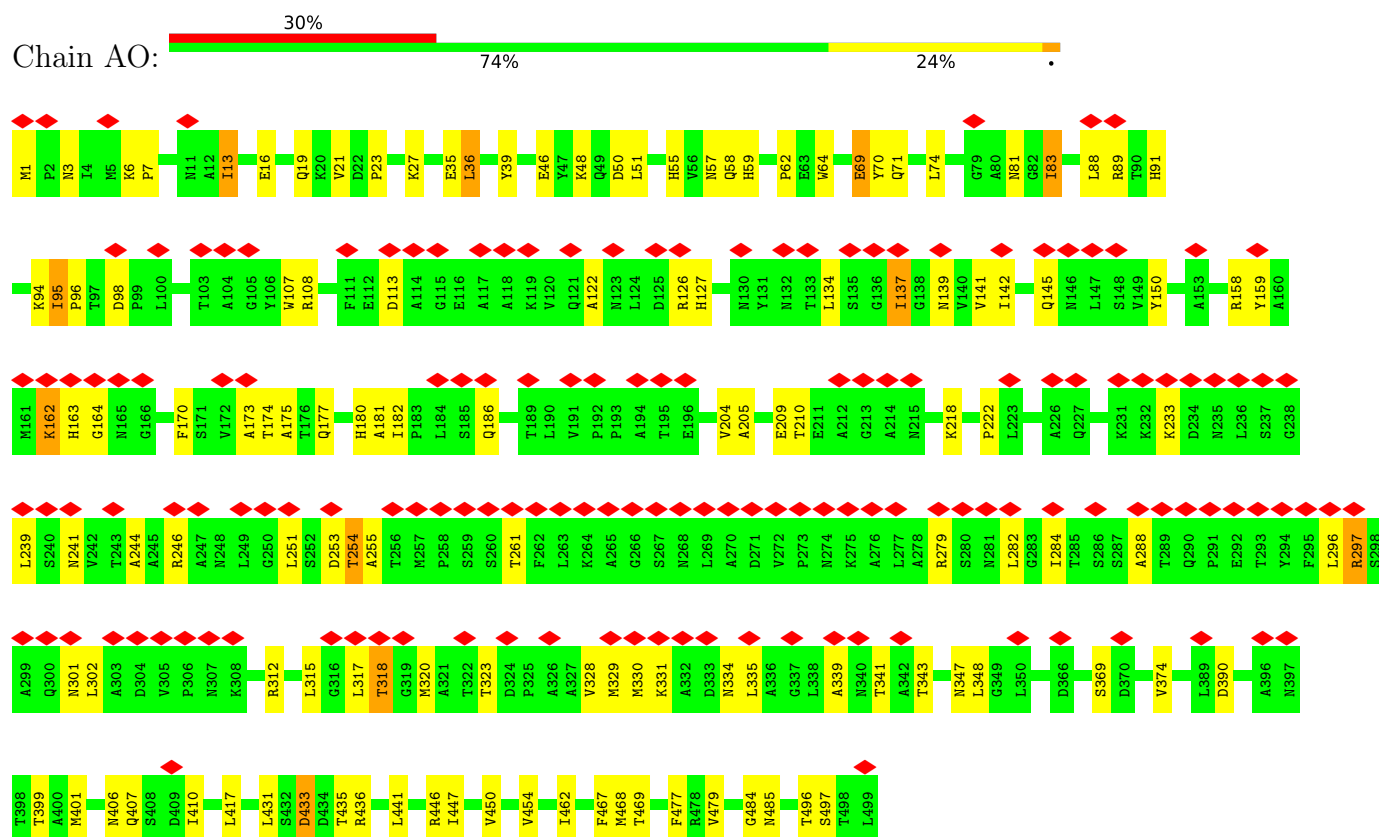
• Molecule 11: short tail fiber gp92

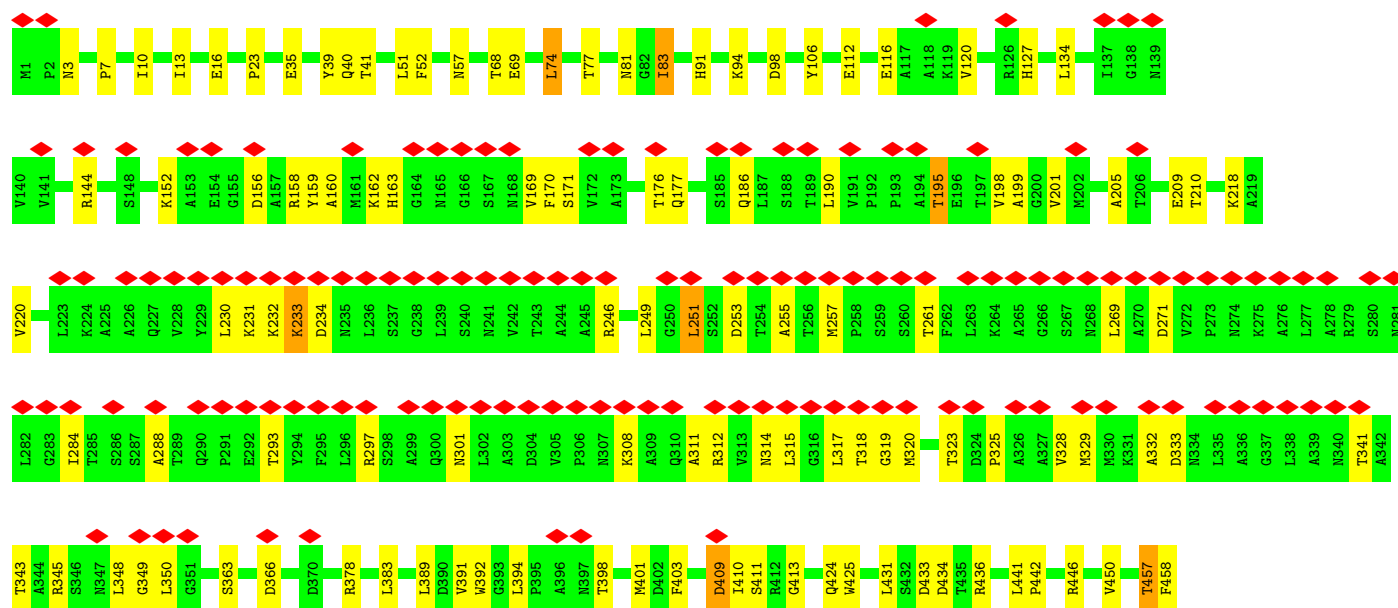


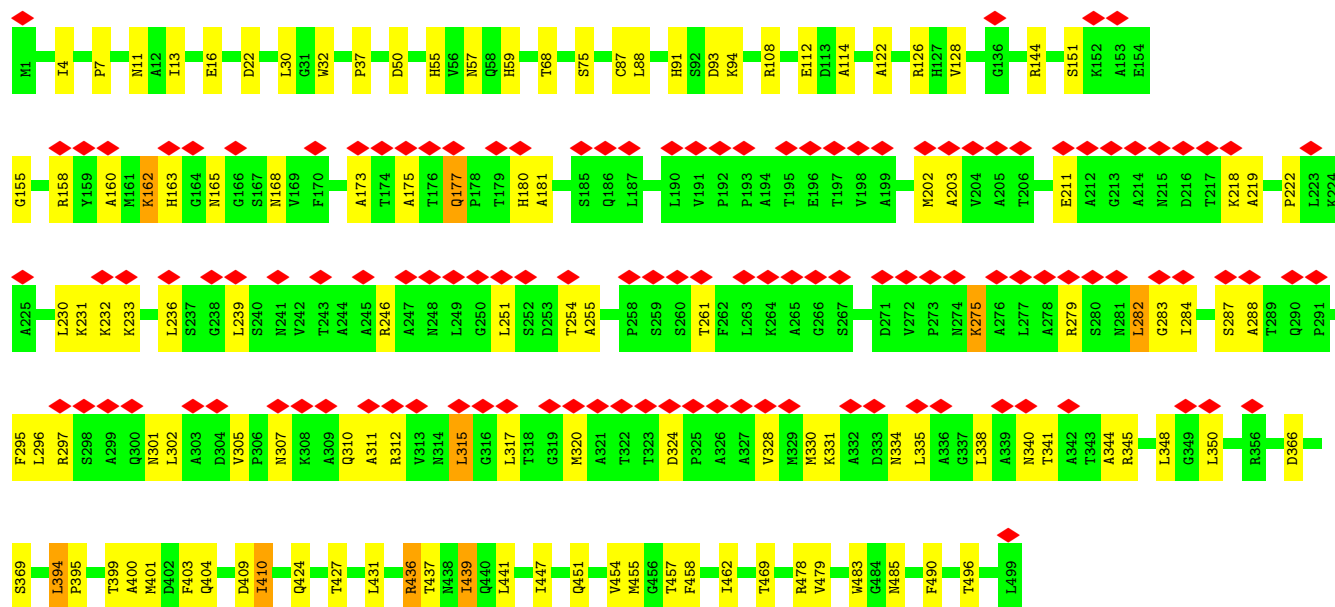
• Molecule 11: short tail fiber gp92



• Molecule 11: short tail fiber gp92







4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	10400	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	1200	Depositor
Maximum defocus (nm)	5000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.085	Depositor
Minimum map value	-0.045	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.004	Depositor
Recommended contour level	0.0202	Depositor
Map size (Å)	697.344, 697.344, 697.344	wwPDB
Map dimensions	512, 512, 512	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.362, 1.362, 1.362	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	0	0.18	0/3747	0.35	0/5117
1	L	0.18	0/3747	0.35	0/5117
1	M	0.19	0/3747	0.37	2/5117 (0.0%)
1	N	0.18	0/3747	0.35	0/5117
1	V	0.18	0/3747	0.35	0/5117
1	W	0.18	0/3747	0.34	0/5117
1	X	0.18	0/3747	0.36	0/5117
1	f	0.18	0/3747	0.36	0/5117
1	g	0.19	0/3747	0.34	0/5117
1	h	0.18	0/3747	0.35	0/5117
1	o	0.18	0/3747	0.36	0/5117
1	u	0.18	0/3747	0.35	0/5117
2	1	0.20	0/1917	0.41	0/2598
2	O	0.18	0/1917	0.39	0/2598
2	Y	0.20	0/1917	0.40	0/2598
2	i	0.19	0/1917	0.39	0/2598
2	p	0.20	0/1917	0.39	0/2598
2	v	0.19	0/1917	0.38	0/2598
3	A	0.25	0/1910	0.40	0/2595
3	B	0.24	0/1910	0.41	1/2595 (0.0%)
3	C	0.25	0/1910	0.42	0/2595
3	D	0.25	0/1910	0.41	0/2595
3	E	0.24	0/1910	0.40	0/2595
3	F	0.25	0/1910	0.43	1/2595 (0.0%)
4	G	0.29	0/1261	0.38	0/1714
4	Q	0.30	0/1261	0.39	0/1714
4	a	0.29	0/1261	0.38	0/1714
4	k	0.29	0/1261	0.37	0/1714
4	q	0.29	0/1261	0.37	0/1714
4	w	0.29	0/1261	0.38	0/1714
5	H	0.29	0/1305	0.40	0/1767
5	R	0.28	0/1305	0.39	0/1767
5	b	0.29	0/1305	0.40	0/1767
5	l	0.29	0/1305	0.41	0/1767

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
5	r	0.29	0/1305	0.39	0/1767
5	x	0.28	0/1305	0.40	0/1767
6	I	0.25	0/984	0.37	0/1342
6	S	0.23	0/984	0.35	0/1342
6	c	0.24	0/984	0.35	0/1342
6	m	0.23	0/984	0.36	0/1342
6	s	0.24	0/984	0.35	0/1342
6	y	0.22	0/984	0.34	0/1342
7	K	0.22	0/1002	0.33	0/1360
7	U	0.21	0/1002	0.32	0/1360
7	e	0.22	0/1002	0.33	0/1360
7	n	0.22	0/1002	0.34	0/1360
7	t	0.22	0/1002	0.34	0/1360
7	z	0.22	0/1002	0.35	0/1360
8	P	0.21	0/1914	0.39	0/2606
8	Z	0.21	0/1914	0.37	0/2606
8	j	0.22	0/1914	0.37	0/2606
9	J	0.24	0/2397	0.41	0/3245
9	T	0.24	0/2397	0.41	0/3245
9	d	0.25	0/2397	0.44	0/3245
10	2	0.18	0/143	0.40	0/194
10	3	0.17	0/143	0.27	0/194
10	4	0.19	0/143	0.37	0/194
10	5	0.17	0/143	0.32	0/194
10	6	0.18	0/143	0.30	0/194
10	7	0.18	0/143	0.41	0/194
10	8	0.21	0/255	0.34	0/341
10	9	0.19	0/255	0.29	0/341
10	AA	0.20	0/255	0.30	0/341
11	AB	0.17	0/3811	0.34	0/5205
11	AC	0.16	0/3811	0.30	0/5205
11	AD	0.15	0/3811	0.31	0/5205
11	AE	0.15	0/3811	0.31	0/5205
11	AF	0.14	0/3811	0.29	0/5205
11	AG	0.13	0/3811	0.29	0/5205
11	AH	0.15	0/3811	0.30	0/5205
11	AI	0.14	0/3811	0.29	0/5205
11	AJ	0.14	0/3811	0.29	0/5205
11	AK	0.17	0/3811	0.37	0/5205
11	AL	0.16	0/3811	0.31	0/5205
11	AM	0.15	0/3811	0.32	0/5205
11	AN	0.14	0/3811	0.30	0/5205
11	AO	0.14	0/3811	0.29	0/5205

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
11	AP	0.13	0/3811	0.29	0/5205
11	AQ	0.16	0/3811	0.30	0/5205
11	AR	0.15	0/3811	0.29	0/5205
11	AS	0.15	0/3811	0.30	0/5205
All	All	0.20	0/178392	0.35	4/243090 (0.0%)

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	F	85	VAL	N-CA-C	-5.70	107.26	112.96
3	B	230	THR	N-CA-C	-5.54	107.16	114.31
1	M	94	HIS	CB-CA-C	-5.33	110.41	116.54
1	M	300	ALA	CB-CA-C	-5.33	109.99	117.23

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts ⓘ

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	0	3681	0	3678	74	0
1	L	3681	0	3678	57	0
1	M	3681	0	3678	81	0
1	N	3681	0	3678	57	0
1	V	3681	0	3678	86	0
1	W	3681	0	3678	72	0
1	X	3681	0	3678	62	0
1	f	3681	0	3678	54	0
1	g	3681	0	3678	80	0
1	h	3681	0	3678	60	0
1	o	3681	0	3678	83	0
1	u	3681	0	3678	43	0
2	1	1879	0	1856	68	0
2	O	1879	0	1856	71	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	Y	1879	0	1856	70	0
2	i	1879	0	1856	68	0
2	p	1879	0	1856	68	0
2	v	1879	0	1856	62	0
3	A	1876	0	1849	27	0
3	B	1876	0	1849	38	0
3	C	1876	0	1849	28	0
3	D	1876	0	1849	30	0
3	E	1876	0	1849	35	0
3	F	1876	0	1849	40	0
4	G	1237	0	1203	23	0
4	Q	1237	0	1203	25	0
4	a	1237	0	1203	26	0
4	k	1237	0	1203	24	0
4	q	1237	0	1203	26	0
4	w	1237	0	1203	24	0
5	H	1281	0	1297	13	0
5	R	1281	0	1297	16	0
5	b	1281	0	1297	17	0
5	l	1281	0	1297	14	0
5	r	1281	0	1297	19	0
5	x	1281	0	1297	17	0
6	I	956	0	915	15	0
6	S	956	0	915	18	0
6	c	956	0	915	16	0
6	m	956	0	915	17	0
6	s	956	0	915	16	0
6	y	956	0	915	17	0
7	K	979	0	969	20	0
7	U	979	0	969	17	0
7	e	979	0	969	16	0
7	n	979	0	969	22	0
7	t	979	0	969	17	0
7	z	979	0	969	21	0
8	P	1874	0	1857	36	0
8	Z	1874	0	1857	31	0
8	j	1874	0	1857	46	0
9	J	2364	0	2343	38	0
9	T	2364	0	2343	50	0
9	d	2364	0	2343	49	0
10	2	143	0	133	0	0
10	3	143	0	133	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
10	4	143	0	133	1	0
10	5	143	0	133	1	0
10	6	143	0	133	2	0
10	7	143	0	133	0	0
10	8	255	0	247	3	0
10	9	255	0	247	1	0
10	AA	255	0	247	2	0
11	AB	3734	0	3667	97	0
11	AC	3734	0	3667	112	0
11	AD	3734	0	3667	108	0
11	AE	3734	0	3667	92	0
11	AF	3734	0	3667	93	0
11	AG	3734	0	3667	84	0
11	AH	3734	0	3667	95	0
11	AI	3734	0	3667	102	0
11	AJ	3734	0	3667	98	0
11	AK	3734	0	3667	111	0
11	AL	3734	0	3667	107	0
11	AM	3734	0	3667	110	0
11	AN	3734	0	3667	78	0
11	AO	3734	0	3667	91	0
11	AP	3734	0	3667	89	0
11	AQ	3734	0	3667	80	0
11	AR	3734	0	3667	104	0
11	AS	3734	0	3667	93	0
All	All	174969	0	172815	2955	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 8.

All (2955) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:1:139:ARG:HH22	1:g:299:GLN:H	1.15	0.89
1:M:299:GLN:H	2:p:139:ARG:HH22	1.22	0.87
11:AR:159:TYR:HB3	11:AS:158:ARG:HG2	1.54	0.87
2:i:176:LYS:HZ2	2:i:177:ILE:H	1.22	0.86
11:AO:328:VAL:HG12	11:AO:329:MET:HG3	1.58	0.84
11:AK:296:LEU:HB3	11:AM:296:LEU:HD12	1.59	0.84
2:i:84:ASN:HA	2:i:91:THR:H	1.42	0.84
11:AF:328:VAL:HG12	11:AF:329:MET:HG3	1.60	0.84

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:v:84:ASN:HA	2:v:91:THR:H	1.43	0.84
11:AC:311:ALA:O	11:AC:315:LEU:HB2	1.77	0.83
1:W:299:GLN:H	2:Y:139:ARG:HH22	1.26	0.83
2:Y:84:ASN:HA	2:Y:91:THR:H	1.43	0.82
11:AH:329:MET:HB3	11:AI:330:MET:H	1.45	0.82
2:O:176:LYS:HZ2	2:O:177:ILE:H	1.24	0.81
11:AQ:114:ALA:HA	11:AS:112:GLU:HB2	1.63	0.81
2:v:109:TRP:HZ3	11:AI:37:PRO:HD2	1.45	0.81
11:AS:307:ASN:HB3	11:AS:310:GLN:HB2	1.63	0.80
11:AH:174:THR:HA	11:AH:183:PRO:HG3	1.64	0.79
11:AK:434:ASP:H	11:AK:482:ASN:HA	1.46	0.79
6:S:102:GLN:HE22	1:o:35:THR:HA	1.47	0.79
11:AN:174:THR:HA	11:AN:183:PRO:HG3	1.63	0.79
6:y:26:ILE:HD12	6:y:28:ARG:HH21	1.47	0.79
8:j:97:ASP:HB3	9:d:166:MET:HG3	1.63	0.78
1:L:443:MET:HE3	1:W:437:ARG:HH21	1.48	0.78
3:B:131:LYS:HD2	7:K:66:PRO:HB3	1.64	0.78
8:P:97:ASP:HB3	9:T:166:MET:HG3	1.65	0.78
9:J:200:THR:HG21	9:J:206:THR:HG22	1.64	0.78
1:h:303:ILE:HG22	1:h:306:SER:H	1.48	0.78
11:AK:329:MET:HG2	11:AL:330:MET:H	1.49	0.77
3:E:208:GLY:H	9:T:69:ASN:HD21	1.30	0.77
9:J:128:LYS:H	9:J:147:GLN:HE22	1.32	0.77
11:AE:174:THR:HA	11:AE:183:PRO:HG3	1.64	0.77
1:N:46:ALA:HB2	7:U:19:ALA:HA	1.66	0.77
11:AE:140:VAL:O	11:AE:144:ARG:HB2	1.84	0.77
11:AR:210:THR:HA	11:AS:222:PRO:HB3	1.66	0.76
1:X:46:ALA:HB2	7:e:19:ALA:HA	1.67	0.76
11:AD:292:GLU:HB3	11:AD:297:ARG:HD2	1.68	0.76
11:AD:436:ARG:HB2	11:AD:478:ARG:HD2	1.67	0.76
9:d:200:THR:HG21	9:d:206:THR:HG22	1.68	0.75
11:AI:328:VAL:HG12	11:AI:329:MET:HG3	1.67	0.75
11:AF:122:ALA:HB1	11:AF:126:ARG:HH22	1.50	0.75
11:AI:122:ALA:HB1	11:AI:126:ARG:HH22	1.50	0.75
1:h:450:VAL:HG12	1:o:436:SER:HB2	1.67	0.75
7:n:35:ILE:HG12	2:p:22:GLN:HE22	1.52	0.75
1:f:412:GLU:HB3	1:f:484:VAL:HB	1.69	0.75
11:AO:122:ALA:HB1	11:AO:126:ARG:HH22	1.51	0.74
11:AH:296:LEU:HB3	11:AJ:296:LEU:HD12	1.69	0.74
11:AE:168:ASN:HD22	11:AF:162:LYS:HE2	1.52	0.74
1:g:121:ILE:HG23	1:g:259:THR:HB	1.69	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:d:128:LYS:H	9:d:147:GLN:HE22	1.34	0.74
11:AH:486:TRP:HE3	11:AH:487:SER:H	1.36	0.74
1:0:144:GLY:HA3	1:0:215:VAL:HG12	1.69	0.73
11:AF:282:LEU:HA	11:AG:275:LYS:HZ2	1.54	0.73
1:u:412:GLU:HB3	1:u:484:VAL:HB	1.71	0.73
11:AK:114:ALA:HA	11:AM:112:GLU:HB2	1.70	0.73
2:O:215:PHE:H	2:O:238:LEU:HA	1.54	0.72
1:0:296:LYS:HE3	3:D:226:ALA:H	1.53	0.72
1:W:156:LEU:H	1:W:176:SER:HB3	1.54	0.72
8:P:202:TRP:HB3	8:Z:208:HIS:HB2	1.69	0.72
4:k:5:VAL:HG21	5:l:108:TRP:HZ3	1.55	0.72
9:T:200:THR:HG21	9:T:206:THR:HG22	1.70	0.72
2:O:86:PHE:HE2	2:O:110:TYR:H	1.38	0.72
2:1:112:VAL:HG22	11:AC:40:GLN:HE22	1.55	0.71
11:AE:486:TRP:HE3	11:AE:487:SER:H	1.38	0.71
1:h:49:ARG:HH12	1:u:28:VAL:HG13	1.55	0.71
11:AL:159:TYR:HB3	11:AM:158:ARG:HG2	1.72	0.71
11:AL:328:VAL:HG12	11:AL:329:MET:HG3	1.73	0.71
1:W:121:ILE:HG23	1:W:259:THR:HB	1.71	0.71
1:o:144:GLY:HA3	1:o:215:VAL:HG12	1.73	0.71
11:AB:235:ASN:HA	11:AD:239:LEU:HD22	1.73	0.71
6:s:82:LEU:HD11	6:s:104:PHE:HB3	1.70	0.71
11:AF:253:ASP:HB2	11:AG:259:SER:HB2	1.73	0.71
11:AC:491:ASN:HD22	11:AC:491:ASN:H	1.35	0.71
6:c:82:LEU:HD11	6:c:104:PHE:HB3	1.72	0.71
6:m:26:ILE:HD12	6:m:28:ARG:HH21	1.56	0.70
1:N:25:ALA:HB1	1:N:47:LEU:HD21	1.71	0.70
1:N:73:ASN:HD21	1:N:75:ALA:HB3	1.56	0.70
2:Y:112:VAL:HG22	11:AR:40:GLN:HE22	1.56	0.70
11:AE:446:ARG:HH21	11:AF:410:ILE:HG23	1.55	0.70
3:B:204:ARG:CZ	6:y:14:ASP:HB3	2.21	0.70
6:S:26:ILE:HD12	6:S:28:ARG:HH21	1.55	0.70
11:AH:305:VAL:HG11	11:AH:311:ALA:HB2	1.74	0.70
11:AI:335:LEU:HD22	11:AJ:335:LEU:HD21	1.74	0.70
3:E:113:GLN:HG3	4:a:151:VAL:HG23	1.74	0.70
9:T:183:CYS:HG	9:T:190:TRP:CD1	2.09	0.70
1:L:412:GLU:HB3	1:L:484:VAL:HB	1.73	0.69
11:AL:321:ALA:HB2	11:AM:321:ALA:HB2	1.73	0.69
11:AR:312:ARG:HG2	11:AR:317:LEU:HD12	1.74	0.69
1:g:437:ARG:HH21	1:u:443:MET:HE3	1.56	0.69
1:f:164:VAL:HB	1:f:167:ILE:HB	1.73	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:AG:297:ARG:HB2	11:AG:300:GLN:HB2	1.74	0.69
11:AN:486:TRP:HE3	11:AN:487:SER:H	1.40	0.69
11:AC:210:THR:HA	11:AD:222:PRO:HB3	1.73	0.69
11:AK:431:LEU:HD11	11:AK:479:VAL:HB	1.72	0.69
1:g:156:LEU:H	1:g:176:SER:HB3	1.56	0.69
1:g:300:ALA:HB1	1:g:306:SER:HB2	1.75	0.69
4:a:5:VAL:HG21	5:b:108:TRP:HZ3	1.58	0.69
11:AC:112:GLU:HB2	11:AD:114:ALA:HA	1.74	0.69
4:w:5:VAL:HG21	5:x:108:TRP:HZ3	1.57	0.69
1:W:202:THR:HG23	1:W:203:LEU:HG	1.75	0.68
11:AC:284:ILE:HD11	11:AD:284:ILE:HD13	1.74	0.68
1:X:303:ILE:HG22	1:X:306:SER:H	1.58	0.68
11:AI:159:TYR:HB3	11:AJ:158:ARG:HG2	1.74	0.68
11:AR:314:ASN:HD22	11:AS:301:ASN:HB2	1.56	0.68
11:AE:436:ARG:HG3	11:AE:478:ARG:HD2	1.75	0.68
2:O:239:THR:HG22	2:O:242:VAL:H	1.58	0.68
11:AB:114:ALA:HA	11:AD:112:GLU:HB2	1.74	0.68
11:AN:168:ASN:HD22	11:AO:162:LYS:HE2	1.58	0.68
1:M:300:ALA:HB1	1:M:306:SER:HB2	1.74	0.68
1:V:397:ILE:HA	1:V:455:ILE:HG22	1.75	0.68
4:Q:41:ARG:HA	4:Q:47:HIS:HD2	1.59	0.68
2:v:176:LYS:HZ2	2:v:177:ILE:H	1.41	0.68
11:AE:296:LEU:HB3	11:AG:296:LEU:HD12	1.76	0.68
3:E:204:ARG:CZ	6:S:14:ASP:HB3	2.24	0.68
7:K:46:LEU:HD11	1:V:18:LEU:HD11	1.76	0.67
1:u:164:VAL:HB	1:u:167:ILE:HB	1.75	0.67
11:AR:51:LEU:HD23	11:AS:7:PRO:HB3	1.75	0.67
8:Z:202:TRP:HB3	8:j:208:HIS:HB2	1.77	0.67
6:I:82:LEU:HD11	6:I:104:PHE:HB3	1.75	0.67
2:Y:109:TRP:H	2:Y:109:TRP:HD1	1.43	0.67
11:AN:339:ALA:H	11:AO:334:ASN:HD21	1.43	0.67
1:0:167:ILE:HD13	1:0:168:ASN:H	1.60	0.67
3:D:34:ILE:HD12	3:D:43:HIS:HD2	1.59	0.67
1:g:105:LEU:HB3	1:g:267:TRP:HE1	1.59	0.67
6:s:44:ASP:HB3	6:s:55:THR:HA	1.76	0.67
1:0:174:TYR:HB3	1:0:191:LEU:HD23	1.77	0.67
1:M:156:LEU:H	1:M:176:SER:HB3	1.60	0.67
1:X:25:ALA:HB1	1:X:47:LEU:HD21	1.76	0.67
11:AL:69:GLU:HG2	11:AL:92:SER:HB3	1.75	0.67
11:AB:330:MET:HE1	11:AD:335:LEU:H	1.59	0.66
8:j:52:LYS:HD2	9:T:187:ASN:HD21	1.61	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:AN:436:ARG:HG3	11:AN:478:ARG:HD2	1.75	0.66
11:AQ:235:ASN:HA	11:AS:239:LEU:HD22	1.77	0.66
3:B:61:ASP:HB2	4:G:48:THR:HG23	1.76	0.66
1:M:121:ILE:HG23	1:M:259:THR:HB	1.77	0.66
2:Y:109:TRP:H	2:Y:109:TRP:CD1	2.13	0.66
7:n:46:LEU:HD11	1:o:18:LEU:HD11	1.77	0.66
11:AE:368:LEU:HD23	11:AE:371:LEU:HD11	1.78	0.66
2:1:108:PRO:HD3	11:AB:36:LEU:HA	1.76	0.66
8:P:2:ARG:HG3	9:J:277:ASN:HD21	1.60	0.66
11:AF:433:ASP:HB2	11:AF:484:GLY:H	1.60	0.66
11:AQ:329:MET:HG2	11:AR:329:MET:HA	1.77	0.66
3:B:176:GLU:HB2	4:Q:43:ILE:HD11	1.78	0.66
1:o:174:TYR:HB3	1:o:191:LEU:HD23	1.78	0.66
7:K:1:MET:HG3	1:V:33:VAL:HG12	1.77	0.66
1:W:73:ASN:HD21	1:W:75:ALA:HB3	1.60	0.66
2:p:109:TRP:CD1	2:p:109:TRP:H	2.13	0.66
1:0:397:ILE:HA	1:0:455:ILE:HG22	1.76	0.66
1:o:49:ARG:HH11	2:p:20:THR:HG21	1.61	0.66
11:AK:427:THR:HG22	11:AK:491:ASN:HB2	1.77	0.66
11:AQ:455:MET:H	11:AQ:490:PHE:HA	1.60	0.66
4:G:5:VAL:HG21	5:H:108:TRP:HZ3	1.61	0.65
11:AB:434:ASP:H	11:AB:482:ASN:HA	1.60	0.65
7:n:1:MET:HG3	1:o:33:VAL:HG12	1.76	0.65
11:AI:253:ASP:HB2	11:AJ:259:SER:HB2	1.78	0.65
11:AN:36:LEU:HD23	11:AN:36:LEU:H	1.60	0.65
3:B:113:GLN:HG3	4:G:151:VAL:HG23	1.76	0.65
1:h:147:ILE:HD11	1:h:160:LEU:HD22	1.78	0.65
11:AI:159:TYR:HB2	11:AJ:160:ALA:H	1.62	0.65
4:Q:5:VAL:HG21	5:R:108:TRP:HZ3	1.60	0.65
11:AI:62:PRO:HG2	11:AJ:57:ASN:HA	1.77	0.65
1:W:298:VAL:H	2:Y:139:ARG:NH2	1.94	0.65
1:f:406:SER:HB2	1:f:447:GLY:HA3	1.78	0.65
11:AF:210:THR:HA	11:AG:222:PRO:HB3	1.79	0.65
11:AC:328:VAL:HG12	11:AC:329:MET:HG3	1.78	0.65
11:AB:305:VAL:HG11	11:AB:311:ALA:HB2	1.77	0.65
4:G:151:VAL:HG13	4:G:154:ALA:HB2	1.78	0.65
1:L:164:VAL:HB	1:L:167:ILE:HB	1.78	0.65
11:AC:320:MET:HB3	11:AD:325:PRO:HB3	1.78	0.65
5:H:146:VAL:HG22	5:x:69:PRO:HB3	1.79	0.65
2:v:109:TRP:CZ3	11:AI:37:PRO:HD2	2.28	0.65
11:AR:363:SER:HB3	11:AR:366:ASP:HB2	1.78	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:M:418:ARG:HD2	1:M:445:ILE:HD11	1.79	0.65
1:V:144:GLY:HA3	1:V:215:VAL:HG12	1.79	0.65
11:AO:253:ASP:HB2	11:AP:259:SER:HB2	1.77	0.65
9:d:183:CYS:HG	9:d:190:TRP:CD1	2.16	0.64
6:S:57:LEU:HB3	6:S:65:ILE:HD11	1.79	0.64
1:W:25:ALA:HB1	1:W:47:LEU:HD21	1.79	0.64
1:W:357:ILE:O	1:W:361:LYS:HB3	1.96	0.64
2:v:239:THR:HG22	2:v:242:VAL:H	1.61	0.64
11:AL:112:GLU:HB2	11:AM:114:ALA:HA	1.78	0.64
11:AS:366:ASP:HB3	11:AS:369:SER:HB3	1.79	0.64
1:M:202:THR:HG23	1:M:203:LEU:HG	1.77	0.64
11:AE:255:ALA:HB1	11:AG:255:ALA:HB2	1.80	0.64
11:AK:288:ALA:HB2	11:AL:288:ALA:HB1	1.78	0.64
1:X:103:VAL:HG12	1:X:272:ASN:HB3	1.80	0.64
11:AI:347:ASN:HB3	11:AJ:336:ALA:HB2	1.80	0.64
11:AH:140:VAL:O	11:AH:144:ARG:HB2	1.98	0.64
11:AK:426:GLY:HA3	11:AK:492:TRP:CE2	2.32	0.64
2:i:134:LYS:HZ1	2:i:138:ASN:HD22	1.45	0.64
2:p:109:TRP:H	2:p:109:TRP:HD1	1.44	0.64
11:AC:69:GLU:HG2	11:AC:92:SER:HB3	1.78	0.64
1:L:34:SER:H	7:U:1:MET:HE3	1.63	0.64
11:AE:236:LEU:HD22	11:AE:239:LEU:HD21	1.80	0.64
11:AF:468:MET:HB3	11:AG:454:VAL:HB	1.80	0.64
1:M:437:ARG:HH12	1:f:446:PRO:HA	1.63	0.64
1:M:456:ALA:HB2	1:M:462:GLN:HA	1.79	0.64
1:W:323:ILE:HD12	1:W:342:LEU:HD23	1.80	0.64
4:k:151:VAL:HG13	4:k:154:ALA:HB2	1.79	0.64
11:AG:69:GLU:HG2	11:AG:92:SER:HB2	1.80	0.64
11:AF:335:LEU:HD22	11:AG:335:LEU:HD21	1.80	0.64
1:O:207:GLU:HA	1:O:212:LEU:HA	1.79	0.63
1:N:147:ILE:HD11	1:N:160:LEU:HD22	1.78	0.63
6:c:54:LEU:HD23	6:c:57:LEU:HD11	1.80	0.63
11:AD:449:ASN:HD21	11:AD:451:GLN:HE21	1.43	0.63
11:AL:210:THR:HA	11:AM:222:PRO:HB3	1.80	0.63
1:W:339:HIS:CE1	2:Y:168:ALA:HB3	2.33	0.63
11:AC:205:ALA:HA	11:AC:218:LYS:HZ2	1.62	0.63
1:o:397:ILE:HA	1:o:455:ILE:HG22	1.81	0.63
11:AI:210:THR:HA	11:AJ:222:PRO:HB3	1.79	0.63
1:M:343:PRO:HG2	1:M:387:TYR:HA	1.81	0.63
1:h:103:VAL:HG12	1:h:272:ASN:HB3	1.78	0.63
11:AS:246:ARG:HG2	11:AS:251:LEU:HD12	1.79	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:v:9:GLU:H	2:v:44:GLN:HE22	1.45	0.63
11:AJ:436:ARG:HG3	11:AJ:478:ARG:HD2	1.80	0.63
3:F:204:ARG:CZ	6:m:14:ASP:HB3	2.28	0.63
1:u:106:GLU:HB3	1:u:269:SER:HB3	1.79	0.63
11:AK:235:ASN:HA	11:AM:239:LEU:HD22	1.80	0.63
7:e:1:MET:HE3	1:f:34:SER:H	1.63	0.63
11:AQ:368:LEU:HD23	11:AQ:371:LEU:HD11	1.81	0.63
2:1:215:PHE:HD1	2:1:236:GLY:HA3	1.64	0.63
11:AI:412:ARG:HG2	11:AI:442:PRO:HG3	1.81	0.63
11:AO:469:THR:HG22	11:AO:479:VAL:HG22	1.80	0.63
2:1:168:ALA:HB3	1:g:339:HIS:CE1	2.34	0.62
3:C:34:ILE:HD12	3:C:43:HIS:HD2	1.63	0.62
11:AG:203:ALA:HB3	11:AG:218:LYS:HG2	1.81	0.62
11:AC:436:ARG:HD2	11:AD:458:PHE:HE2	1.64	0.62
11:AH:312:ARG:HG2	11:AH:317:LEU:HD12	1.81	0.62
11:AL:51:LEU:HD23	11:AM:7:PRO:HB3	1.81	0.62
11:AS:312:ARG:HG2	11:AS:317:LEU:HD22	1.80	0.62
1:o:207:GLU:HA	1:o:212:LEU:HA	1.81	0.62
11:AE:71:GLN:HA	11:AE:90:THR:HG22	1.82	0.62
11:AF:64:TRP:CD1	11:AF:70:TYR:HH	2.16	0.62
11:AK:441:LEU:HD23	11:AK:476:GLY:HA2	1.80	0.62
11:AQ:177:GLN:HB2	11:AQ:180:HIS:CE1	2.34	0.62
1:0:118:ALA:HA	1:0:262:ILE:HG21	1.79	0.62
4:k:41:ARG:HA	4:k:47:HIS:HD2	1.64	0.62
11:AJ:69:GLU:HG2	11:AJ:92:SER:HB2	1.81	0.62
2:1:22:GLN:HE22	7:z:35:ILE:HG12	1.64	0.62
2:p:81:ASP:HB3	2:p:84:ASN:HB3	1.82	0.62
11:AD:366:ASP:HB3	11:AD:369:SER:HB3	1.80	0.62
11:AK:427:THR:HA	11:AK:491:ASN:HA	1.82	0.62
1:g:456:ALA:HB2	1:g:462:GLN:HA	1.82	0.62
1:h:298:VAL:H	2:v:139:ARG:NH2	1.97	0.62
7:t:1:MET:HE3	1:u:34:SER:H	1.63	0.62
2:v:139:ARG:CZ	2:v:139:ARG:HA	2.30	0.62
1:X:298:VAL:H	2:i:139:ARG:NH2	1.97	0.62
8:j:96:MET:HE1	8:j:122:ILE:HD11	1.82	0.62
11:AH:236:LEU:HD22	11:AH:239:LEU:HD21	1.81	0.62
11:AO:347:ASN:HB3	11:AP:336:ALA:HB2	1.82	0.62
8:P:93:GLN:HE22	8:j:22:TYR:HA	1.65	0.62
11:AB:58:GLN:HE22	11:AC:3:ASN:HA	1.65	0.62
11:AC:431:LEU:HD11	11:AC:437:THR:HG22	1.82	0.62
11:AH:463:GLY:H	11:AJ:483:TRP:HB2	1.65	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:p:209:PHE:HB3	2:p:241:LEU:HB2	1.80	0.62
11:AG:436:ARG:HG3	11:AG:478:ARG:HD2	1.80	0.62
1:M:391:VAL:HB	1:M:473:GLU:HG3	1.82	0.62
1:N:303:ILE:HG22	1:N:306:SER:H	1.64	0.62
8:Z:22:TYR:HA	8:j:93:GLN:HE22	1.63	0.62
11:AC:338:LEU:HA	11:AD:331:LYS:HE2	1.80	0.62
11:AH:168:ASN:HD22	11:AI:162:LYS:HE2	1.64	0.62
11:AS:203:ALA:HB3	11:AS:218:LYS:HG2	1.80	0.62
1:u:406:SER:HB2	1:u:447:GLY:HA3	1.80	0.62
9:T:226:PRO:HB2	9:T:269:LEU:HD12	1.82	0.62
11:AB:464:PRO:HG2	11:AD:466:ALA:HB3	1.81	0.62
1:N:103:VAL:HG12	1:N:272:ASN:HB3	1.81	0.61
2:O:9:GLU:H	2:O:44:GLN:HE22	1.48	0.61
11:AE:78:GLN:HE21	11:AE:82:GLY:HA2	1.65	0.61
11:AB:177:GLN:HB2	11:AB:180:HIS:CE1	2.35	0.61
11:AM:246:ARG:HG2	11:AM:251:LEU:HD12	1.80	0.61
1:N:106:GLU:HG2	1:N:237:ARG:HG2	1.82	0.61
1:V:156:LEU:HB3	1:V:230:ASN:HD22	1.65	0.61
1:W:418:ARG:HD2	1:W:445:ILE:HD11	1.81	0.61
1:g:202:THR:HG23	1:g:203:LEU:HG	1.82	0.61
11:AN:297:ARG:HB2	11:AN:300:GLN:HB2	1.82	0.61
3:F:34:ILE:HD11	3:F:40:ILE:HB	1.81	0.61
1:X:73:ASN:HD21	1:X:75:ALA:HB3	1.64	0.61
1:g:418:ARG:HD2	1:g:445:ILE:HD11	1.83	0.61
11:AN:78:GLN:HE21	11:AN:82:GLY:HA2	1.65	0.61
2:O:88:PHE:N	2:O:109:TRP:HB3	2.14	0.61
8:P:110:PRO:HD3	8:j:48:ASN:HB2	1.82	0.61
1:g:343:PRO:HG2	1:g:387:TYR:HA	1.81	0.61
11:AH:436:ARG:HG3	11:AH:478:ARG:HD2	1.82	0.61
11:AL:433:ASP:HB2	11:AL:484:GLY:H	1.65	0.61
1:M:25:ALA:HB1	1:M:47:LEU:HD21	1.81	0.61
1:M:298:VAL:H	2:p:139:ARG:NH2	1.98	0.61
1:W:456:ALA:HB2	1:W:462:GLN:HA	1.81	0.61
11:AR:68:THR:HA	11:AS:11:ASN:HD21	1.66	0.61
8:Z:155:LEU:HA	8:Z:160:GLU:HG2	1.82	0.61
11:AH:329:MET:HB3	11:AI:330:MET:N	2.14	0.61
2:1:109:TRP:CD1	2:1:109:TRP:H	2.19	0.61
4:a:143:VAL:HA	5:b:86:MET:HE2	1.83	0.61
4:a:151:VAL:HG13	4:a:154:ALA:HB2	1.83	0.61
4:q:151:VAL:HG13	4:q:154:ALA:HB2	1.82	0.61
11:AN:305:VAL:HG11	11:AN:311:ALA:HB2	1.81	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:b:135:MET:HE3	5:b:137:ILE:HG12	1.83	0.61
11:AB:439:ILE:HD13	11:AB:440:GLN:H	1.66	0.61
1:0:33:VAL:HG12	7:z:1:MET:HG2	1.81	0.61
1:W:343:PRO:HG2	1:W:387:TYR:HA	1.83	0.61
7:n:41:LEU:HA	7:n:51:GLY:HA3	1.83	0.61
11:AH:255:ALA:HB1	11:AJ:255:ALA:HB2	1.83	0.61
11:AH:446:ARG:HH21	11:AI:410:ILE:HG23	1.64	0.61
11:AI:433:ASP:HB2	11:AI:484:GLY:H	1.65	0.61
11:AN:43:ASN:HD21	11:AP:32:TRP:H	1.47	0.61
11:AP:233:LYS:H	11:AP:233:LYS:NZ	1.99	0.61
9:J:32:LEU:HD11	9:J:85:LYS:HD2	1.83	0.61
11:AK:151:SER:HB3	11:AK:154:GLU:HG3	1.83	0.61
5:b:69:PRO:HG3	5:l:141:VAL:HG11	1.83	0.60
1:g:391:VAL:HB	1:g:473:GLU:HG3	1.83	0.60
11:AS:345:ARG:HG2	11:AS:350:LEU:HD12	1.83	0.60
7:K:41:LEU:HA	7:K:51:GLY:HA3	1.82	0.60
1:M:437:ARG:HH21	1:f:443:MET:HE3	1.66	0.60
1:X:156:LEU:H	1:X:176:SER:HB3	1.66	0.60
9:T:75:TYR:HA	9:T:97:VAL:HG23	1.83	0.60
11:AP:69:GLU:HG2	11:AP:92:SER:HB2	1.81	0.60
11:AQ:230:LEU:HB2	11:AS:230:LEU:HD11	1.82	0.60
11:AS:469:THR:HG22	11:AS:479:VAL:HG22	1.84	0.60
1:0:18:LEU:HD11	7:z:46:LEU:HD11	1.82	0.60
1:N:249:PRO:HA	1:N:279:GLY:H	1.66	0.60
1:h:456:ALA:HB2	1:h:462:GLN:HA	1.83	0.60
11:AN:263:LEU:HB3	11:AP:263:LEU:HD12	1.84	0.60
1:0:159:GLU:HB2	1:0:173:LYS:HE2	1.83	0.60
1:L:161:LYS:HB3	1:L:163:TYR:HE1	1.66	0.60
1:M:357:ILE:O	1:M:361:LYS:HB3	2.01	0.60
1:h:359:LEU:HD21	1:u:300:ALA:HB1	1.83	0.60
8:j:8:GLU:HG2	9:T:51:LYS:HD2	1.84	0.60
1:o:156:LEU:HB3	1:o:230:ASN:HD22	1.66	0.60
11:AE:297:ARG:HB2	11:AE:300:GLN:HB2	1.82	0.60
11:AK:258:PRO:HG2	11:AK:261:THR:HG21	1.83	0.60
8:P:1:MET:HA	9:J:232:SER:HB3	1.84	0.60
3:D:56:VAL:HG12	3:D:185:GLN:HG2	1.83	0.60
1:V:396:GLU:HA	1:V:481:ASP:HB3	1.84	0.60
2:i:239:THR:HG22	2:i:242:VAL:H	1.67	0.60
2:p:215:PHE:HD1	2:p:236:GLY:HA3	1.65	0.60
11:AC:51:LEU:HD23	11:AD:7:PRO:HB3	1.84	0.60
3:A:2:THR:HG23	4:Q:46:HIS:HD2	1.67	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:107:PHE:HD2	3:A:111:ILE:HG13	1.66	0.60
1:V:158:TYR:HE1	1:V:176:SER:HB3	1.67	0.60
1:g:11:ILE:HG21	1:g:66:GLN:HB2	1.84	0.60
1:g:86:VAL:HG21	1:g:288:LEU:HD21	1.83	0.60
11:AC:315:LEU:HB3	11:AC:317:LEU:HG	1.84	0.60
11:AO:62:PRO:HG2	11:AP:57:ASN:HA	1.83	0.60
1:N:156:LEU:H	1:N:176:SER:HB3	1.67	0.60
1:N:298:VAL:H	2:O:139:ARG:NH2	2.00	0.60
1:f:106:GLU:HB3	1:f:269:SER:HB3	1.84	0.60
2:1:139:ARG:NH2	1:g:298:VAL:H	2.00	0.60
4:G:53:ARG:HH22	4:Q:44:ARG:HB3	1.67	0.60
1:M:86:VAL:HG21	1:M:288:LEU:HD21	1.84	0.60
2:Y:81:ASP:HB3	2:Y:84:ASN:HB3	1.84	0.60
4:a:62:GLU:HG2	4:a:124:VAL:HG22	1.84	0.60
1:h:298:VAL:H	2:v:139:ARG:HH21	1.50	0.60
3:E:23:ARG:HB2	3:E:51:PHE:HD1	1.66	0.60
1:V:174:TYR:HB3	1:V:191:LEU:HD23	1.83	0.60
1:g:73:ASN:HD21	1:g:75:ALA:HB3	1.65	0.60
1:o:111:THR:HG21	1:o:266:GLY:HA3	1.84	0.60
1:o:396:GLU:HA	1:o:481:ASP:HB3	1.84	0.60
11:AD:13:ILE:HG23	11:AD:50:ASP:HB3	1.84	0.60
11:AK:483:TRP:CG	11:AL:463:GLY:H	2.20	0.60
11:AR:152:LYS:O	11:AR:156:ASP:HB2	2.02	0.60
3:C:176:GLU:HB3	4:q:43:ILE:HD11	1.84	0.59
4:q:143:VAL:HA	5:r:86:MET:HE2	1.84	0.59
11:AC:320:MET:HG3	11:AD:320:MET:O	2.02	0.59
11:AP:436:ARG:HG3	11:AP:478:ARG:HD2	1.84	0.59
1:M:11:ILE:HG21	1:M:66:GLN:HB2	1.82	0.59
5:R:69:PRO:HB3	5:b:146:VAL:HG22	1.83	0.59
1:W:391:VAL:HB	1:W:473:GLU:HG3	1.83	0.59
11:AD:267:SER:HB2	11:AD:270:ALA:HB3	1.83	0.59
11:AD:279:ARG:HB3	11:AD:284:ILE:HB	1.83	0.59
2:1:21:GLU:HA	2:1:24:LYS:HG3	1.84	0.59
1:L:437:ARG:HH22	1:W:447:GLY:H	1.50	0.59
6:c:33:TYR:HE1	1:o:11:ILE:HD11	1.66	0.59
1:h:299:GLN:H	2:v:139:ARG:NH2	2.00	0.59
2:i:88:PHE:HB2	2:i:95:GLY:H	1.66	0.59
11:AK:230:LEU:HB2	11:AM:230:LEU:HD11	1.85	0.59
11:AK:463:GLY:H	11:AM:483:TRP:HB2	1.67	0.59
3:A:34:ILE:HD12	3:A:43:HIS:HD2	1.68	0.59
2:O:139:ARG:CZ	2:O:139:ARG:HA	2.33	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:X:330:PRO:HB3	1:X:337:PRO:HA	1.83	0.59
11:AO:210:THR:HA	11:AP:222:PRO:HB3	1.85	0.59
1:M:323:ILE:HD12	1:M:342:LEU:HD23	1.83	0.59
4:k:75:SER:O	4:k:79:GLN:HG2	2.02	0.59
11:AL:328:VAL:HG13	11:AM:330:MET:HG3	1.84	0.59
2:i:139:ARG:HA	2:i:139:ARG:CZ	2.32	0.59
9:T:13:GLY:HA2	9:T:77:THR:HG23	1.84	0.59
9:d:13:GLY:HA2	9:d:77:THR:HG23	1.83	0.59
11:AF:91:HIS:CE1	11:AF:94:LYS:HB2	2.37	0.59
11:AH:302:LEU:HD11	11:AJ:302:LEU:HD11	1.85	0.59
11:AK:305:VAL:HG11	11:AK:311:ALA:HB2	1.85	0.59
11:AQ:315:LEU:HD13	11:AS:315:LEU:HD21	1.84	0.59
11:AS:13:ILE:HG23	11:AS:50:ASP:HB3	1.84	0.59
1:o:112:VAL:HG13	1:o:136:ILE:HG12	1.85	0.59
11:AQ:32:TRP:HZ3	11:AQ:37:PRO:HB3	1.67	0.59
11:AQ:278:ALA:HB1	11:AR:269:LEU:HD12	1.84	0.59
5:r:69:PRO:HG3	5:x:141:VAL:HG11	1.83	0.59
11:AH:75:SER:HB2	11:AH:87:CYS:HB3	1.85	0.59
1:f:304:LEU:HD11	1:f:322:ILE:HG13	1.84	0.59
1:f:325:ASN:HD21	1:f:338:GLY:HA2	1.67	0.59
1:g:25:ALA:HB1	1:g:47:LEU:HD21	1.84	0.59
11:AK:435:THR:HG22	11:AK:436:ARG:H	1.67	0.59
11:AK:453:THR:HG21	11:AM:452:VAL:H	1.67	0.59
11:AN:236:LEU:HD22	11:AN:239:LEU:HD21	1.85	0.59
1:N:91:ILE:HB	1:N:291:ARG:HH22	1.67	0.59
1:X:147:ILE:HD11	1:X:160:LEU:HD22	1.84	0.59
7:n:1:MET:HE3	1:o:34:SER:H	1.68	0.59
2:p:21:GLU:HA	2:p:24:LYS:HG3	1.85	0.59
2:p:87:GLY:HA3	2:p:109:TRP:HA	1.84	0.59
11:AB:332:ALA:HB1	11:AB:335:LEU:HG	1.85	0.59
11:AB:441:LEU:HD11	11:AB:447:ILE:HD11	1.85	0.59
11:AL:378:ARG:HG3	11:AL:383:LEU:HD12	1.85	0.59
11:AO:64:TRP:CD1	11:AO:70:TYR:HH	2.20	0.59
11:AO:433:ASP:HB2	11:AO:484:GLY:H	1.68	0.59
4:G:97:GLY:HA3	4:G:140:ASN:HD22	1.67	0.58
1:X:106:GLU:HG2	1:X:237:ARG:HG2	1.84	0.58
11:AB:75:SER:HB2	11:AB:87:CYS:HB3	1.84	0.58
11:AK:177:GLN:HB2	11:AK:180:HIS:CE1	2.38	0.58
11:AN:75:SER:HB2	11:AN:87:CYS:HB3	1.85	0.58
11:AO:205:ALA:HB1	11:AO:209:GLU:HB2	1.84	0.58
11:AQ:297:ARG:HA	11:AS:295:PHE:HA	1.85	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:M:403:ASN:HA	1:M:407:MET:HE1	1.84	0.58
1:g:323:ILE:HD12	1:g:342:LEU:HD23	1.85	0.58
2:i:108:PRO:HB3	11:AN:35:GLU:C	2.28	0.58
11:AK:91:HIS:CE1	11:AK:94:LYS:HB2	2.38	0.58
11:AN:81:ASN:HD21	11:AN:85:TYR:HE2	1.49	0.58
6:y:57:LEU:HB3	6:y:65:ILE:HD11	1.86	0.58
11:AC:246:ARG:HB3	11:AC:251:LEU:HD12	1.85	0.58
11:AK:288:ALA:HB1	11:AM:284:ILE:HG23	1.84	0.58
5:H:15:ALA:HA	5:H:90:PRO:HG2	1.85	0.58
1:V:293:ARG:HE	1:V:296:LYS:HZ1	1.49	0.58
1:o:321:ARG:HH21	1:o:323:ILE:HD11	1.67	0.58
2:v:77:LEU:HA	2:v:122:PRO:HD3	1.84	0.58
7:z:63:ARG:HH11	7:z:63:ARG:HA	1.68	0.58
11:AE:89:ARG:HD2	11:AE:106:TYR:HE1	1.67	0.58
11:AC:250:GLY:HA3	11:AD:246:ARG:HH22	1.68	0.58
11:AK:330:MET:HE1	11:AM:335:LEU:H	1.69	0.58
1:M:93:ARG:HG2	1:M:283:GLU:HB3	1.84	0.58
2:Y:85:TYR:HA	2:Y:117:GLY:N	2.19	0.58
5:l:69:PRO:HG3	5:r:141:VAL:HG11	1.85	0.58
1:u:188:LEU:HB3	1:u:212:LEU:HD12	1.86	0.58
1:h:91:ILE:HB	1:h:291:ARG:HH22	1.68	0.58
11:AB:91:HIS:CE1	11:AB:94:LYS:HB2	2.39	0.58
11:AQ:320:MET:HG2	11:AR:325:PRO:HB3	1.86	0.58
1:N:456:ALA:HB2	1:N:462:GLN:HA	1.86	0.58
4:Q:75:SER:O	4:Q:79:GLN:HG2	2.04	0.58
11:AH:368:LEU:HD23	11:AH:371:LEU:HD11	1.85	0.58
11:AH:441:LEU:HD11	11:AH:447:ILE:HD11	1.86	0.58
11:AR:284:ILE:HG23	11:AS:288:ALA:HB1	1.85	0.58
1:0:211:ILE:HD13	1:0:234:GLN:HG3	1.84	0.58
2:1:109:TRP:H	2:1:109:TRP:HD1	1.51	0.58
11:AO:159:TYR:HB3	11:AP:158:ARG:HG2	1.85	0.58
11:AR:40:GLN:NE2	11:AR:40:GLN:H	2.01	0.58
1:0:49:ARG:HE	2:1:20:THR:HG21	1.69	0.58
3:E:176:GLU:HB2	4:k:43:ILE:HD11	1.86	0.58
11:AI:91:HIS:CE1	11:AI:94:LYS:HB2	2.38	0.58
11:AI:469:THR:HG22	11:AI:479:VAL:HG22	1.86	0.58
1:W:249:PRO:HA	1:W:279:GLY:H	1.69	0.57
1:W:389:ARG:HD3	1:W:390:PRO:HD2	1.86	0.57
1:h:156:LEU:H	1:h:176:SER:HB3	1.69	0.57
1:h:249:PRO:HA	1:h:279:GLY:H	1.69	0.57
5:x:135:MET:HE3	5:x:137:ILE:HG12	1.86	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:AF:239:LEU:HD22	11:AG:235:ASN:HA	1.86	0.57
11:AP:32:TRP:CH2	11:AP:37:PRO:HB3	2.39	0.57
11:AF:205:ALA:HB1	11:AF:209:GLU:HB2	1.86	0.57
11:AK:51:LEU:HD23	11:AL:7:PRO:HB3	1.86	0.57
11:AO:239:LEU:HD22	11:AP:235:ASN:HA	1.86	0.57
5:H:135:MET:HE3	5:H:137:ILE:HG12	1.85	0.57
11:AK:320:MET:HE2	11:AL:325:PRO:HA	1.86	0.57
1:W:307:LEU:HD11	1:W:357:ILE:HD13	1.86	0.57
1:g:307:LEU:HD11	1:g:357:ILE:HD13	1.85	0.57
9:T:242:ARG:HH22	9:d:75:TYR:HE2	1.52	0.57
11:AE:1:MET:HE2	11:AG:58:GLN:HE21	1.68	0.57
11:AB:36:LEU:HD22	11:AB:36:LEU:H	1.68	0.57
11:AJ:203:ALA:HB3	11:AJ:218:LYS:HG2	1.85	0.57
11:AO:91:HIS:CE1	11:AO:94:LYS:HB2	2.38	0.57
3:F:131:LYS:HD2	7:z:66:PRO:HB3	1.87	0.57
1:M:73:ASN:HD21	1:M:75:ALA:HB3	1.70	0.57
1:X:299:GLN:HE22	1:f:300:ALA:HA	1.70	0.57
7:z:41:LEU:HA	7:z:51:GLY:HA3	1.85	0.57
11:AE:177:GLN:HB2	11:AE:180:HIS:CE1	2.39	0.57
11:AM:13:ILE:HG23	11:AM:50:ASP:HB3	1.87	0.57
11:AS:305:VAL:HG11	11:AS:311:ALA:HB2	1.87	0.57
2:1:84:ASN:HA	2:1:90:GLY:HA2	1.86	0.57
1:M:339:HIS:CE1	2:p:168:ALA:HB3	2.40	0.57
4:q:32:TRP:HZ3	4:q:132:TRP:HE1	1.53	0.57
11:AF:159:TYR:CG	11:AG:160:ALA:HB3	2.40	0.57
11:AC:461:SER:C	11:AC:485:ASN:HD22	2.13	0.57
11:AI:13:ILE:HG12	11:AI:50:ASP:HB3	1.86	0.57
11:AP:338:LEU:HD23	11:AP:339:ALA:H	1.70	0.57
2:O:77:LEU:HA	2:O:122:PRO:HD3	1.87	0.57
1:X:91:ILE:HB	1:X:291:ARG:HH22	1.70	0.57
8:Z:60:PRO:HB2	9:J:170:GLN:HG3	1.87	0.57
4:a:60:ARG:HG2	4:a:126:THR:HG22	1.85	0.57
4:w:62:GLU:HG2	4:w:124:VAL:HG22	1.86	0.57
5:x:39:ILE:HG13	10:4:695:GLN:HE22	1.68	0.57
11:AF:62:PRO:HG2	11:AG:57:ASN:HA	1.87	0.57
11:AF:279:ARG:HB3	11:AF:284:ILE:HB	1.87	0.57
11:AL:450:VAL:HG13	11:AL:494:ALA:HB2	1.86	0.57
4:q:53:ARG:HH22	4:w:44:ARG:HB3	1.69	0.57
6:y:11:LEU:HD12	6:y:101:PRO:HA	1.86	0.57
11:AP:203:ALA:HB3	11:AP:218:LYS:HG2	1.86	0.57
3:F:113:GLN:HG3	4:q:151:VAL:HG23	1.87	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:N:299:GLN:H	2:O:139:ARG:NH2	2.02	0.57
2:O:108:PRO:HD3	11:AE:36:LEU:HD22	1.87	0.57
1:o:49:ARG:NH1	2:p:20:THR:HG21	2.20	0.57
1:o:397:ILE:HB	1:o:482:ILE:HA	1.85	0.57
11:AG:338:LEU:HD23	11:AG:339:ALA:H	1.70	0.57
11:AB:427:THR:HG22	11:AB:491:ASN:HB2	1.87	0.57
11:AC:40:GLN:NE2	11:AC:40:GLN:H	2.02	0.57
11:AC:254:THR:HG23	11:AD:259:SER:HA	1.87	0.57
11:AI:139:ASN:HB3	11:AI:142:ILE:HB	1.86	0.57
11:AI:182:ILE:HD11	11:AJ:184:LEU:HA	1.86	0.57
11:AE:246:ARG:HG2	11:AE:251:LEU:HD12	1.86	0.56
11:AB:390:ASP:HB3	11:AC:400:ALA:HB2	1.87	0.56
11:AR:343:THR:HB	11:AS:334:ASN:HD22	1.70	0.56
1:O:112:VAL:HG13	1:O:136:ILE:HG12	1.86	0.56
1:N:330:PRO:HB3	1:N:337:PRO:HA	1.87	0.56
2:O:110:TYR:HB3	11:AF:39:TYR:HD2	1.71	0.56
1:W:11:ILE:HG21	1:W:66:GLN:HB2	1.88	0.56
1:X:456:ALA:HB2	1:X:462:GLN:HA	1.87	0.56
1:O:407:MET:HB2	1:O:448:PHE:HB3	1.86	0.56
9:J:228:TYR:CZ	9:T:72:GLU:HG3	2.41	0.56
11:AD:300:GLN:HB3	11:AD:303:ALA:HB3	1.87	0.56
11:AH:469:THR:HG22	11:AH:479:VAL:HG22	1.87	0.56
11:AI:468:MET:HB3	11:AJ:454:VAL:HB	1.86	0.56
11:AJ:436:ARG:H	11:AJ:436:ARG:HD2	1.69	0.56
11:AO:282:LEU:HA	11:AP:275:LYS:HZ2	1.69	0.56
11:AO:468:MET:HB3	11:AP:454:VAL:HB	1.86	0.56
11:AS:455:MET:HG3	11:AS:490:PHE:HA	1.87	0.56
1:O:115:SER:HB2	1:O:131:LEU:HB2	1.87	0.56
3:A:79:ILE:HG22	3:A:81:ASN:H	1.68	0.56
3:F:214:LYS:HE2	9:d:300:GLN:HB3	1.87	0.56
1:N:104:VAL:HG12	1:N:239:LEU:HD23	1.87	0.56
2:Y:21:GLU:HA	2:Y:24:LYS:HG3	1.87	0.56
2:p:108:PRO:HD3	11:AK:36:LEU:HD13	1.88	0.56
11:AB:328:VAL:HB	11:AB:332:ALA:HB2	1.88	0.56
11:AK:390:ASP:HB3	11:AL:400:ALA:HB2	1.86	0.56
11:AR:378:ARG:HG3	11:AR:383:LEU:HD12	1.86	0.56
1:N:147:ILE:HD12	1:N:231:LEU:HD13	1.87	0.56
11:AB:230:LEU:HB2	11:AD:230:LEU:HD11	1.88	0.56
11:AI:174:THR:HG23	11:AI:186:GLN:HE22	1.70	0.56
11:AK:159:TYR:N	11:AL:162:LYS:HB2	2.21	0.56
11:AM:202:MET:HG2	11:AM:219:ALA:HB2	1.87	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:AN:329:MET:HB3	11:AO:330:MET:H	1.70	0.56
3:B:34:ILE:HD11	3:B:40:ILE:HB	1.88	0.56
3:F:208:GLY:H	9:J:69:ASN:HD21	1.53	0.56
8:P:8:GLU:HG2	9:J:51:LYS:HD2	1.87	0.56
5:b:116:SER:H	5:b:124:ARG:HH12	1.51	0.56
1:h:73:ASN:HD21	1:h:75:ALA:HB3	1.69	0.56
2:p:84:ASN:HA	2:p:90:GLY:HA2	1.87	0.56
7:z:2:ASP:HB3	7:z:31:GLN:HE22	1.70	0.56
11:AE:463:GLY:H	11:AG:483:TRP:HB2	1.69	0.56
1:h:330:PRO:HB3	1:h:337:PRO:HA	1.88	0.56
11:AB:458:PHE:HB3	11:AD:436:ARG:HH22	1.69	0.56
11:AN:144:ARG:HA	11:AN:147:LEU:HB2	1.87	0.56
11:AP:436:ARG:H	11:AP:436:ARG:HD2	1.69	0.56
4:a:115:THR:HB	4:a:121:GLU:CD	2.31	0.56
11:AB:296:LEU:HB3	11:AD:296:LEU:HD12	1.88	0.56
11:AC:320:MET:HE3	11:AD:320:MET:HA	1.88	0.56
11:AH:309:ALA:HA	11:AH:312:ARG:HE	1.71	0.56
11:AN:483:TRP:CG	11:AO:462:ILE:HG23	2.41	0.56
11:AF:36:LEU:HD13	11:AF:37:PRO:HD2	1.87	0.56
11:AQ:51:LEU:HD23	11:AR:7:PRO:HB3	1.88	0.56
5:H:141:VAL:HG11	5:x:69:PRO:HG3	1.87	0.56
7:t:40:PHE:HB2	7:t:43:GLU:CD	2.30	0.56
9:d:203:ASN:HA	9:d:274:ARG:NH1	2.21	0.56
11:AH:159:TYR:N	11:AI:162:LYS:HB2	2.20	0.56
11:AS:436:ARG:HG3	11:AS:478:ARG:HD2	1.88	0.56
4:G:120:ILE:HG23	5:b:51:VAL:HG11	1.87	0.55
2:O:110:TYR:CD1	11:AF:39:TYR:HB3	2.41	0.55
2:Y:27:PRO:O	2:Y:31:ARG:HG2	2.06	0.55
11:AQ:436:ARG:HG3	11:AQ:478:ARG:HD2	1.88	0.55
11:AR:328:VAL:HG12	11:AR:329:MET:HG3	1.88	0.55
1:O:111:THR:HG21	1:O:266:GLY:HA3	1.87	0.55
3:C:56:VAL:HG12	3:C:185:GLN:HG2	1.88	0.55
1:L:410:ASN:OD1	2:Y:116:THR:HG21	2.05	0.55
2:O:184:SER:O	2:O:189:LEU:HB2	2.06	0.55
1:X:342:LEU:HD13	1:X:368:VAL:HG23	1.88	0.55
2:Y:117:GLY:O	2:Y:118:ASN:HB2	2.07	0.55
5:l:69:PRO:HB3	5:r:146:VAL:HG22	1.88	0.55
2:p:107:ALA:HA	11:AK:36:LEU:HD13	1.88	0.55
3:F:24:GLN:HE21	3:F:26:ARG:HD3	1.71	0.55
6:S:11:LEU:HD12	6:S:101:PRO:HA	1.88	0.55
1:W:127:ARG:HH21	1:W:246:VAL:HB	1.71	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:u:73:ASN:HB3	1:u:76:ALA:HB3	1.88	0.55
11:AB:468:MET:O	11:AB:479:VAL:HG13	2.06	0.55
7:K:52:ILE:HD11	7:K:75:GLU:HG2	1.89	0.55
1:W:393:VAL:HG13	1:W:475:ALA:HA	1.87	0.55
2:v:184:SER:O	2:v:189:LEU:HB2	2.06	0.55
11:AB:78:GLN:HE21	11:AB:82:GLY:HA2	1.70	0.55
11:AN:177:GLN:HB2	11:AN:180:HIS:CE1	2.42	0.55
1:M:172:ILE:HD13	1:M:195:VAL:HG22	1.88	0.55
11:AD:88:LEU:HD11	11:AD:108:ARG:HB3	1.89	0.55
11:AO:51:LEU:HD23	11:AP:7:PRO:HB3	1.87	0.55
1:O:17:ILE:HD13	1:O:58:ASP:HB3	1.88	0.55
2:O:177:ILE:HB	2:O:210:GLN:HE21	1.71	0.55
8:P:230:LYS:HE2	8:j:243:VAL:HG12	1.88	0.55
1:V:111:THR:HG21	1:V:266:GLY:HA3	1.89	0.55
8:Z:96:MET:HE1	8:Z:122:ILE:HD11	1.88	0.55
4:q:5:VAL:HG21	5:r:108:TRP:HZ3	1.70	0.55
2:v:88:PHE:H	2:v:88:PHE:HD2	1.54	0.55
1:V:207:GLU:HA	1:V:212:LEU:HA	1.87	0.55
1:X:299:GLN:H	2:i:139:ARG:NH2	2.05	0.55
1:h:147:ILE:HD12	1:h:231:LEU:HD13	1.89	0.55
1:o:118:ALA:HA	1:o:262:ILE:HG21	1.88	0.55
11:AL:232:LYS:HB3	11:AL:233:LYS:HZ2	1.72	0.55
11:AM:433:ASP:HB2	11:AM:484:GLY:H	1.71	0.55
4:G:60:ARG:HG2	4:G:126:THR:HG22	1.88	0.55
1:V:397:ILE:HB	1:V:482:ILE:HA	1.88	0.55
1:g:253:GLN:HA	1:h:148:PHE:CZ	2.42	0.55
6:m:57:LEU:HB3	6:m:65:ILE:HD11	1.88	0.55
11:AC:36:LEU:HD22	11:AC:36:LEU:H	1.71	0.55
11:AJ:300:GLN:HE22	11:AJ:304:ASP:HB3	1.70	0.55
3:D:79:ILE:HG22	3:D:81:ASN:H	1.69	0.55
3:D:113:GLN:HB2	4:w:151:VAL:HG23	1.88	0.55
1:W:158:TYR:HE1	1:W:176:SER:HB2	1.70	0.55
1:W:300:ALA:HB1	1:W:306:SER:HB2	1.89	0.55
5:l:88:LYS:HB3	5:l:106:THR:HG23	1.88	0.55
2:p:100:LEU:HG	11:AK:40:GLN:HG3	1.89	0.55
2:v:112:VAL:HG22	11:AI:38:PRO:HB2	1.88	0.55
11:AB:435:THR:HG22	11:AB:436:ARG:H	1.71	0.55
11:AH:272:VAL:HG11	11:AH:278:ALA:HB2	1.88	0.55
11:AL:246:ARG:HB3	11:AL:251:LEU:HD12	1.89	0.55
11:AO:13:ILE:HG12	11:AO:50:ASP:HB3	1.89	0.55
3:F:124:VAL:HG21	4:k:79:GLN:HB2	1.89	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:S:69:TYR:HE2	1:X:80:VAL:HG13	1.72	0.55
8:Z:212:TYR:HB3	8:j:219:SER:HA	1.89	0.55
1:o:391:VAL:HB	1:o:473:GLU:HG2	1.88	0.55
1:u:304:LEU:HD11	1:u:322:ILE:HG13	1.87	0.55
11:AN:461:SER:HG	11:AN:486:TRP:CD1	2.25	0.55
1:f:162:MET:H	1:f:171:SER:HA	1.72	0.54
2:p:214:VAL:HA	2:p:239:THR:HB	1.89	0.54
11:AE:144:ARG:HA	11:AE:147:LEU:HB2	1.88	0.54
11:AC:434:ASP:HA	11:AD:458:PHE:CG	2.42	0.54
1:0:158:TYR:HE1	1:0:176:SER:HB3	1.72	0.54
1:M:393:VAL:HG13	1:M:475:ALA:HA	1.87	0.54
7:n:63:ARG:HA	7:n:63:ARG:HH11	1.72	0.54
9:d:32:LEU:HD11	9:d:85:LYS:HD2	1.89	0.54
11:AN:441:LEU:HD11	11:AN:447:ILE:HD11	1.88	0.54
11:AN:463:GLY:H	11:AP:483:TRP:HB2	1.72	0.54
11:AS:338:LEU:HD23	11:AS:344:ALA:HB2	1.89	0.54
2:1:108:PRO:HG3	11:AB:35:GLU:C	2.33	0.54
6:c:86:ASN:HD21	6:c:88:GLU:HB3	1.72	0.54
1:g:393:VAL:HG13	1:g:475:ALA:HA	1.88	0.54
1:g:458:LYS:HZ2	1:g:459:GLY:H	1.55	0.54
7:n:52:ILE:HD11	7:n:75:GLU:HG2	1.88	0.54
11:AB:96:PRO:HG3	11:AB:107:TRP:CE2	2.42	0.54
11:AI:51:LEU:HD23	11:AJ:7:PRO:HB3	1.87	0.54
11:AK:57:ASN:HD21	11:AM:68:THR:HG21	1.72	0.54
1:L:399:ILE:HB	1:L:484:VAL:HG13	1.90	0.54
2:O:84:ASN:HA	2:O:91:THR:H	1.72	0.54
1:g:161:LYS:H	1:g:228:ALA:HB2	1.71	0.54
2:v:108:PRO:HB3	11:AH:35:GLU:O	2.08	0.54
11:AE:329:MET:HB3	11:AF:330:MET:H	1.72	0.54
11:AB:288:ALA:HB1	11:AD:284:ILE:HG23	1.88	0.54
2:i:84:ASN:C	2:i:117:GLY:HA2	2.33	0.54
11:AD:345:ARG:HG2	11:AD:350:LEU:HD12	1.90	0.54
11:AH:220:VAL:HG13	11:AI:222:PRO:HG3	1.90	0.54
11:AQ:91:HIS:CE1	11:AQ:94:LYS:HB2	2.41	0.54
5:H:12:VAL:HG22	5:H:93:ILE:HG12	1.89	0.54
8:P:115:LYS:HZ2	8:j:19:SER:HA	1.73	0.54
1:h:393:VAL:HG23	1:h:475:ALA:HA	1.90	0.54
1:o:154:ASN:HB3	1:o:178:ALA:HA	1.89	0.54
11:AE:305:VAL:HG11	11:AE:311:ALA:HB2	1.90	0.54
11:AK:484:GLY:HA2	11:AK:488:TYR:CE2	2.43	0.54
11:AM:469:THR:HG22	11:AM:479:VAL:HG22	1.90	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:E:24:GLN:HE21	3:E:26:ARG:HD3	1.72	0.54
1:L:174:TYR:HB3	1:L:191:LEU:HG	1.90	0.54
1:V:188:LEU:HA	1:V:191:LEU:HD12	1.89	0.54
8:j:67:VAL:HA	8:j:123:ALA:HB3	1.88	0.54
4:k:115:THR:HG23	4:q:29:GLU:HG2	1.88	0.54
11:AF:127:HIS:CD2	11:AG:128:VAL:HG22	2.43	0.54
11:AH:288:ALA:HA	11:AJ:287:SER:HB2	1.90	0.54
11:AH:380:ASN:HD21	11:AI:369:SER:HA	1.72	0.54
11:AI:401:MET:HE1	11:AJ:401:MET:HE1	1.90	0.54
11:AL:338:LEU:HA	11:AM:331:LYS:HE2	1.88	0.54
1:0:443:MET:HE3	1:N:437:ARG:NE	2.23	0.54
1:W:458:LYS:HZ2	1:W:459:GLY:H	1.55	0.54
2:i:184:SER:O	2:i:189:LEU:HB2	2.08	0.54
11:AF:182:ILE:HD11	11:AG:184:LEU:HA	1.90	0.54
11:AB:223:LEU:HG	11:AB:227:GLN:HE22	1.72	0.54
11:AD:469:THR:HG22	11:AD:479:VAL:HG22	1.90	0.54
11:AR:159:TYR:HB2	11:AS:160:ALA:H	1.72	0.54
1:o:303:ILE:H	1:o:303:ILE:HD12	1.73	0.54
2:v:88:PHE:N	2:v:109:TRP:HB3	2.23	0.54
9:J:72:GLU:HG3	9:d:228:TYR:CZ	2.43	0.54
11:AN:264:LYS:HA	11:AP:262:PHE:HA	1.89	0.54
7:e:12:LEU:H	7:e:12:LEU:HD12	1.73	0.53
1:h:290:GLU:HA	1:h:293:ARG:HH21	1.74	0.53
9:J:75:TYR:HE2	9:d:242:ARG:HH22	1.54	0.53
11:AI:205:ALA:HB1	11:AI:209:GLU:HB2	1.90	0.53
11:AR:394:LEU:HD13	11:AR:398:THR:HG21	1.89	0.53
1:0:34:SER:H	7:z:1:MET:HE2	1.73	0.53
1:o:293:ARG:HH21	1:o:296:LYS:HE3	1.73	0.53
11:AE:264:LYS:HA	11:AG:262:PHE:HA	1.89	0.53
11:AH:331:LYS:HE2	11:AJ:328:VAL:HG12	1.90	0.53
11:AN:220:VAL:HG13	11:AO:222:PRO:HG3	1.90	0.53
6:I:28:ARG:HH22	6:I:74:ILE:HG22	1.74	0.53
1:V:154:ASN:HB3	1:V:178:ALA:HA	1.90	0.53
4:a:53:ARG:HH22	4:k:44:ARG:HB3	1.72	0.53
1:o:211:ILE:HG23	1:o:234:GLN:CD	2.33	0.53
9:J:242:ARG:HH22	9:T:75:TYR:HE2	1.55	0.53
11:AE:263:LEU:HB3	11:AG:263:LEU:HD12	1.88	0.53
11:AK:236:LEU:HD21	11:AM:236:LEU:HD22	1.91	0.53
11:AL:213:GLY:HA3	11:AM:226:ALA:HB2	1.90	0.53
11:AN:144:ARG:HH12	11:AP:148:SER:HB3	1.71	0.53
11:AR:159:TYR:CE1	11:AS:160:ALA:HB3	2.43	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:O:11:ILE:HD11	6:s:33:TYR:HE2	1.73	0.53
11:AR:320:MET:HE2	11:AS:320:MET:HB3	1.91	0.53
3:E:61:ASP:HB2	4:a:48:THR:HG23	1.91	0.53
6:I:13:GLN:HE22	6:I:98:ASP:HA	1.73	0.53
11:AK:331:LYS:HG2	11:AM:328:VAL:HB	1.91	0.53
11:AN:58:GLN:HE21	11:AO:1:MET:HE2	1.73	0.53
2:1:117:GLY:O	2:1:118:ASN:HB2	2.09	0.53
3:B:207:LYS:HA	9:d:69:ASN:HD21	1.72	0.53
1:W:387:TYR:HE2	1:W:389:ARG:HH12	1.56	0.53
2:i:110:TYR:CD1	11:AO:39:TYR:HB3	2.43	0.53
1:o:161:LYS:HB2	1:o:226:GLU:HB2	1.90	0.53
11:AE:159:TYR:N	11:AF:162:LYS:HB2	2.24	0.53
11:AG:436:ARG:H	11:AG:436:ARG:HD2	1.73	0.53
11:AN:1:MET:HB2	11:AO:69:GLU:HB3	1.90	0.53
11:AN:222:PRO:HG2	11:AP:215:ASN:HB3	1.89	0.53
11:AP:297:ARG:HB2	11:AP:300:GLN:HB2	1.91	0.53
3:A:147:ALA:HB3	9:T:34:ARG:HH12	1.74	0.53
7:K:63:ARG:HA	7:K:63:ARG:HH11	1.73	0.53
1:L:31:ASP:HA	6:s:103:PHE:HE1	1.73	0.53
4:w:76:LEU:HD11	4:w:88:ILE:HD13	1.91	0.53
11:AF:412:ARG:HG2	11:AF:442:PRO:HG3	1.91	0.53
11:AJ:446:ARG:HH12	11:AJ:499:LEU:HD23	1.73	0.53
11:AM:307:ASN:HB3	11:AM:310:GLN:HG2	1.91	0.53
1:O:290:GLU:O	1:O:294:ASN:HB2	2.09	0.53
1:O:397:ILE:HB	1:O:482:ILE:HA	1.90	0.53
3:E:23:ARG:HB2	3:E:51:PHE:CD1	2.44	0.53
1:V:88:PHE:HE1	2:Y:56:LEU:HB2	1.74	0.53
1:h:31:ASP:HB2	2:v:31:ARG:NH2	2.23	0.53
11:AH:177:GLN:HB2	11:AH:180:HIS:CE1	2.44	0.53
11:AI:328:VAL:HG13	11:AJ:330:MET:HG3	1.91	0.53
11:AK:302:LEU:HD11	11:AM:302:LEU:HD11	1.91	0.53
2:1:185:LEU:HA	2:1:189:LEU:HD22	1.91	0.53
1:X:104:VAL:HG12	1:X:239:LEU:HD23	1.91	0.53
8:Z:240:VAL:HG12	8:j:232:GLY:HA2	1.90	0.53
7:e:114:LEU:H	7:e:114:LEU:HD12	1.74	0.53
2:v:175:GLY:HA2	2:v:209:PHE:CZ	2.44	0.53
11:AI:241:ASN:HB3	11:AI:244:ALA:HB3	1.90	0.53
11:AO:159:TYR:CG	11:AP:160:ALA:HB3	2.43	0.53
11:AS:177:GLN:HB2	11:AS:180:HIS:CE1	2.44	0.53
11:AS:279:ARG:HB3	11:AS:284:ILE:HB	1.89	0.53
2:1:110:TYR:CD1	11:AC:39:TYR:HB3	2.44	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:Z:212:TYR:HE1	8:Z:214:GLN:HB2	1.74	0.53
2:p:110:TYR:CD1	11:AL:39:TYR:HB3	2.44	0.53
11:AC:23:PRO:HG3	11:AC:41:THR:HG23	1.91	0.53
6:I:34:TRP:HE1	6:I:36:SER:HA	1.73	0.52
2:Y:209:PHE:HA	2:Y:239:THR:HB	1.91	0.52
2:Y:240:ASN:HA	2:Y:243:THR:HB	1.90	0.52
11:AC:378:ARG:HG3	11:AC:383:LEU:HD12	1.90	0.52
11:AH:330:MET:O	11:AJ:329:MET:HB3	2.08	0.52
3:A:171:ASP:HB3	3:A:189:THR:HB	1.92	0.52
5:H:51:VAL:HG11	4:q:120:ILE:HG23	1.89	0.52
8:P:93:GLN:HE22	8:j:22:TYR:HD1	1.56	0.52
1:V:211:ILE:HG23	1:V:234:GLN:CD	2.35	0.52
2:Y:210:GLN:HE21	2:Y:239:THR:HG22	1.73	0.52
2:i:137:LYS:NZ	2:i:194:ALA:H	2.08	0.52
11:AF:177:GLN:HB2	11:AF:180:HIS:CE1	2.44	0.52
11:AM:177:GLN:HB2	11:AM:180:HIS:CE1	2.44	0.52
11:AN:7:PRO:HB3	11:AP:51:LEU:HD23	1.91	0.52
6:m:11:LEU:HD12	6:m:101:PRO:HA	1.90	0.52
11:AE:320:MET:HB2	11:AF:325:PRO:HB3	1.90	0.52
3:F:208:GLY:N	9:J:69:ASN:HD21	2.07	0.52
1:M:307:LEU:HD11	1:M:357:ILE:HD13	1.90	0.52
6:S:77:ASN:HB2	6:S:110:ASN:HD21	1.74	0.52
6:y:54:LEU:HD11	6:y:71:MET:HE3	1.89	0.52
7:z:52:ILE:HD11	7:z:75:GLU:HG2	1.91	0.52
11:AK:308:LYS:H	11:AK:308:LYS:HD3	1.74	0.52
11:AK:454:VAL:HG22	11:AK:467:PHE:HE2	1.74	0.52
1:V:112:VAL:HG13	1:V:136:ILE:HG12	1.91	0.52
1:V:118:ALA:HA	1:V:262:ILE:HG21	1.91	0.52
1:X:11:ILE:HG21	1:X:66:GLN:HB2	1.91	0.52
1:X:54:VAL:HG21	2:i:36:LEU:HD12	1.91	0.52
1:X:393:VAL:HG23	1:X:475:ALA:HA	1.91	0.52
1:g:437:ARG:HH12	1:u:446:PRO:HA	1.73	0.52
1:u:363:PHE:HZ	2:v:162:LEU:HD11	1.75	0.52
11:AB:279:ARG:HG2	11:AB:284:ILE:HD12	1.92	0.52
11:AD:406:ASN:HB3	11:AD:414:TRP:NE1	2.25	0.52
11:AQ:96:PRO:HG3	11:AQ:107:TRP:CE2	2.43	0.52
1:L:73:ASN:HB3	1:L:76:ALA:HB3	1.90	0.52
1:M:253:GLN:HA	1:X:148:PHE:CZ	2.45	0.52
1:M:297:PHE:CE1	2:p:138:ASN:HA	2.44	0.52
1:o:290:GLU:O	1:o:294:ASN:HB2	2.10	0.52
4:q:117:THR:HG23	4:q:119:GLY:H	1.75	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:V:407:MET:HG3	1:V:448:PHE:HB3	1.90	0.52
11:AH:483:TRP:CG	11:AI:462:ILE:HG23	2.45	0.52
11:AK:484:GLY:HA2	11:AK:488:TYR:CZ	2.45	0.52
1:L:158:TYR:HE2	1:L:187:ILE:HD13	1.75	0.52
1:M:449:GLN:HG3	1:f:434:ILE:HG21	1.91	0.52
5:R:69:PRO:HG3	5:b:141:VAL:HG11	1.90	0.52
7:t:114:LEU:H	7:t:114:LEU:HD12	1.75	0.52
2:v:137:LYS:NZ	2:v:194:ALA:H	2.08	0.52
9:T:73:THR:HB	9:T:76:LEU:HD21	1.92	0.52
11:AE:7:PRO:HB3	11:AG:51:LEU:HD23	1.90	0.52
11:AN:368:LEU:HD23	11:AN:371:LEU:HD11	1.92	0.52
11:AO:279:ARG:HB3	11:AO:284:ILE:HB	1.91	0.52
3:A:56:VAL:HG12	3:A:185:GLN:HG2	1.92	0.52
8:P:1:MET:H3	8:P:1:MET:HE3	1.75	0.52
1:V:443:MET:HE3	1:X:437:ARG:NE	2.25	0.52
1:X:359:LEU:HD21	1:f:300:ALA:HB1	1.91	0.52
11:AC:177:GLN:HB2	11:AC:180:HIS:CE1	2.45	0.52
11:AH:263:LEU:HD12	11:AI:263:LEU:HB3	1.92	0.52
11:AI:64:TRP:CH2	11:AI:95:ILE:HG12	2.45	0.52
11:AK:425:TRP:HA	11:AK:493:PHE:HA	1.90	0.52
1:O:156:LEU:HB3	1:O:230:ASN:HD22	1.75	0.52
3:A:176:GLU:HA	3:A:180:THR:HG21	1.91	0.52
1:L:262:ILE:HD12	1:L:263:PRO:HD2	1.92	0.52
2:Y:100:LEU:HG	11:AQ:40:GLN:HG3	1.92	0.52
2:Y:215:PHE:HD1	2:Y:236:GLY:HA3	1.75	0.52
1:h:299:GLN:O	1:h:301:THR:HG23	2.10	0.52
1:o:213:PHE:HE2	1:o:235:LYS:HB2	1.75	0.52
6:s:47:ASP:HB3	6:s:53:ILE:HD11	1.91	0.52
9:J:43:ILE:HG12	9:J:56:ALA:HB1	1.92	0.52
11:AH:78:GLN:HE21	11:AH:82:GLY:HA2	1.75	0.52
11:AH:144:ARG:HA	11:AH:147:LEU:HB2	1.92	0.52
11:AL:159:TYR:CE1	11:AM:160:ALA:HB3	2.45	0.52
11:AQ:305:VAL:HG11	11:AQ:311:ALA:HB2	1.92	0.52
11:AR:112:GLU:HB2	11:AS:114:ALA:HA	1.91	0.52
11:AR:315:LEU:HD11	11:AS:302:LEU:HB2	1.91	0.52
1:O:208:GLN:HB3	1:O:213:PHE:HE1	1.75	0.51
1:M:458:LYS:HZ2	1:M:459:GLY:H	1.57	0.51
1:g:132:LEU:HB3	1:g:241:ILE:HG23	1.91	0.51
11:AG:231:LYS:HB2	11:AG:234:ASP:HB2	1.92	0.51
11:AB:51:LEU:HD23	11:AC:7:PRO:HB3	1.92	0.51
11:AD:177:GLN:HB2	11:AD:180:HIS:CE1	2.45	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:AK:144:ARG:HH11	11:AK:151:SER:HB2	1.75	0.51
11:AO:182:ILE:HD11	11:AP:184:LEU:HA	1.90	0.51
3:E:208:GLY:N	9:T:69:ASN:HD21	2.03	0.51
8:Z:22:TYR:HA	8:j:93:GLN:NE2	2.23	0.51
2:v:84:ASN:C	2:v:117:GLY:HA2	2.36	0.51
11:AK:430:GLY:HA2	11:AK:488:TYR:O	2.10	0.51
2:O:91:THR:HG22	2:O:92:GLU:H	1.74	0.51
5:r:135:MET:HE3	5:r:137:ILE:HG12	1.93	0.51
11:AH:159:TYR:H	11:AI:162:LYS:HB2	1.75	0.51
11:AL:91:HIS:CE1	11:AL:94:LYS:HB2	2.45	0.51
11:AL:424:GLN:HG2	11:AL:442:PRO:HD2	1.92	0.51
1:W:28:VAL:HG12	2:Y:31:ARG:NH2	2.25	0.51
9:T:235:ALA:HB3	9:T:242:ARG:HE	1.75	0.51
11:AF:241:ASN:HB3	11:AF:244:ALA:HB3	1.91	0.51
11:AG:427:THR:HA	11:AG:491:ASN:HA	1.92	0.51
11:AD:165:ASN:H	11:AD:168:ASN:ND2	2.08	0.51
11:AJ:427:THR:HA	11:AJ:491:ASN:HA	1.93	0.51
11:AK:298:SER:H	11:AM:295:PHE:HA	1.75	0.51
11:AM:394:LEU:HD13	11:AM:395:PRO:HD2	1.92	0.51
11:AR:461:SER:HB3	11:AR:485:ASN:HD21	1.76	0.51
1:O:154:ASN:HB3	1:O:178:ALA:HA	1.92	0.51
2:1:147:VAL:HG22	2:1:197:PRO:HG2	1.93	0.51
3:A:113:GLN:HB2	4:Q:151:VAL:HG23	1.92	0.51
1:g:407:MET:HE2	1:g:448:PHE:HB3	1.93	0.51
11:AF:318:THR:HG22	11:AF:319:GLY:H	1.76	0.51
11:AQ:296:LEU:HB3	11:AS:296:LEU:HD12	1.91	0.51
1:O:391:VAL:HB	1:O:473:GLU:HG2	1.91	0.51
1:O:396:GLU:HA	1:O:481:ASP:HB3	1.93	0.51
3:B:137:GLU:HB2	3:B:184:LEU:HD11	1.92	0.51
3:F:10:GLY:O	3:F:80:ASN:HB2	2.11	0.51
6:c:28:ARG:HH22	6:c:74:ILE:HG22	1.75	0.51
1:g:434:ILE:HB	1:g:437:ARG:HB2	1.92	0.51
11:AH:134:LEU:HD11	11:AJ:137:ILE:HD13	1.93	0.51
11:AH:263:LEU:HB3	11:AJ:263:LEU:HD12	1.93	0.51
11:AO:64:TRP:CH2	11:AO:95:ILE:HG12	2.46	0.51
11:AR:424:GLN:HE22	11:AR:441:LEU:HB3	1.76	0.51
1:O:74:PRO:HG3	1:O:85:LEU:HD21	1.93	0.51
3:A:34:ILE:HD12	3:A:43:HIS:CD2	2.46	0.51
2:Y:147:VAL:HG22	2:Y:197:PRO:HG2	1.93	0.51
1:h:437:ARG:NE	1:o:443:MET:HE3	2.25	0.51
2:i:83:PHE:O	2:i:91:THR:HA	2.11	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:o:188:LEU:HA	1:o:191:LEU:HD12	1.92	0.51
2:p:85:TYR:HA	2:p:117:GLY:N	2.25	0.51
9:J:226:PRO:HB2	9:J:269:LEU:HD12	1.91	0.51
3:E:124:VAL:HG21	4:Q:79:GLN:HB2	1.92	0.51
1:M:387:TYR:HE2	1:M:389:ARG:HH12	1.57	0.51
1:M:437:ARG:HA	1:M:437:ARG:HE	1.75	0.51
2:O:137:LYS:NZ	2:O:194:ALA:H	2.09	0.51
2:Y:104:THR:HA	2:Y:180:ASN:ND2	2.26	0.51
2:p:73:ARG:HB2	2:p:134:LYS:HG2	1.92	0.51
11:AC:320:MET:HE2	11:AD:323:THR:H	1.74	0.51
11:AH:55:HIS:CE1	11:AI:6:LYS:HB2	2.46	0.51
11:AN:279:ARG:CZ	11:AP:283:GLY:HA3	2.40	0.51
3:C:107:PHE:HD2	3:C:111:ILE:HG13	1.76	0.51
6:S:54:LEU:HD11	6:S:71:MET:HE3	1.92	0.51
1:f:310:GLY:O	1:f:314:VAL:HG23	2.11	0.51
2:i:107:ALA:HB1	2:i:108:PRO:HD2	1.92	0.51
2:v:67:ILE:O	2:v:71:VAL:HG22	2.11	0.51
11:AH:331:LYS:HG3	11:AJ:328:VAL:HB	1.93	0.51
11:AL:159:TYR:HD1	11:AL:160:ALA:N	2.09	0.51
1:N:298:VAL:H	2:O:139:ARG:HH21	1.59	0.51
1:g:387:TYR:HE2	1:g:389:ARG:HH12	1.59	0.51
1:o:207:GLU:HB2	1:o:212:LEU:HD12	1.93	0.51
2:v:84:ASN:HA	2:v:91:THR:N	2.20	0.51
9:T:32:LEU:HD11	9:T:85:LYS:HG3	1.93	0.51
11:AO:177:GLN:HB2	11:AO:180:HIS:CE1	2.47	0.51
11:AO:282:LEU:HD23	11:AP:275:LYS:HZ2	1.76	0.51
11:AQ:433:ASP:HB2	11:AQ:484:GLY:H	1.76	0.51
1:X:31:ASP:HB2	2:i:31:ARG:NH2	2.26	0.50
5:x:88:LYS:HB3	5:x:106:THR:HG23	1.91	0.50
11:AP:233:LYS:H	11:AP:233:LYS:HZ2	1.59	0.50
11:AP:333:ASP:HB3	11:AP:336:ALA:HB3	1.93	0.50
2:1:109:TRP:HE3	11:AC:36:LEU:HD12	1.76	0.50
11:AE:305:VAL:HG13	11:AF:301:ASN:HA	1.92	0.50
11:AC:68:THR:HA	11:AD:11:ASN:HD21	1.75	0.50
11:AL:68:THR:HA	11:AM:11:ASN:HD21	1.76	0.50
11:AL:392:TRP:HB3	11:AM:404:GLN:HG3	1.91	0.50
11:AP:231:LYS:HB2	11:AP:234:ASP:HB2	1.93	0.50
1:O:88:PHE:HE1	2:1:56:LEU:HB2	1.76	0.50
8:P:232:GLY:HA2	8:j:240:VAL:HG12	1.93	0.50
4:k:15:ILE:HG12	4:k:92:VAL:HG12	1.94	0.50
11:AF:13:ILE:HG12	11:AF:50:ASP:HB3	1.93	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:AF:139:ASN:HB3	11:AF:142:ILE:HB	1.93	0.50
11:AB:57:ASN:HD21	11:AD:68:THR:HG21	1.77	0.50
11:AB:330:MET:HB3	11:AD:329:MET:HB2	1.93	0.50
11:AC:491:ASN:HD22	11:AC:491:ASN:N	2.07	0.50
11:AH:33:VAL:HG23	11:AH:35:GLU:HG3	1.93	0.50
11:AI:159:TYR:CG	11:AJ:160:ALA:HB3	2.45	0.50
11:AR:253:ASP:O	11:AR:257:MET:HG3	2.12	0.50
3:C:34:ILE:HD12	3:C:43:HIS:CD2	2.46	0.50
4:G:29:GLU:HG2	4:w:115:THR:HG23	1.93	0.50
4:G:74:PHE:CZ	4:Q:136:THR:HA	2.46	0.50
1:L:75:ALA:HA	1:L:289:ARG:HD3	1.94	0.50
7:U:63:ARG:HA	7:U:63:ARG:HH11	1.76	0.50
1:h:299:GLN:HE22	1:u:300:ALA:HA	1.76	0.50
8:j:32:VAL:HA	8:j:41:VAL:HG12	1.94	0.50
6:y:34:TRP:HE1	6:y:36:SER:HA	1.76	0.50
9:T:43:ILE:HG12	9:T:56:ALA:HB1	1.92	0.50
11:AE:222:PRO:HG2	11:AG:215:ASN:HB3	1.94	0.50
11:AF:64:TRP:CH2	11:AF:95:ILE:HG12	2.47	0.50
11:AC:392:TRP:HB3	11:AD:404:GLN:HG3	1.93	0.50
11:AC:392:TRP:O	11:AD:403:PHE:HB2	2.12	0.50
11:AM:406:ASN:HB3	11:AM:414:TRP:NE1	2.26	0.50
3:B:207:LYS:HA	9:d:69:ASN:ND2	2.27	0.50
3:D:32:ASN:ND2	9:J:38:GLN:HG2	2.26	0.50
1:N:469:ILE:HG23	1:N:473:GLU:HG3	1.93	0.50
1:f:298:VAL:HG23	1:f:299:GLN:H	1.77	0.50
5:r:12:VAL:HG22	5:r:93:ILE:HG12	1.94	0.50
1:u:298:VAL:HG23	1:u:299:GLN:H	1.76	0.50
9:d:43:ILE:HG12	9:d:56:ALA:HB1	1.94	0.50
11:AE:223:LEU:HG	11:AE:227:GLN:HE22	1.76	0.50
11:AC:315:LEU:HD22	11:AC:317:LEU:HD11	1.93	0.50
11:AC:363:SER:HB3	11:AC:366:ASP:HB2	1.93	0.50
11:AJ:338:LEU:HD23	11:AJ:339:ALA:H	1.75	0.50
11:AL:363:SER:HB3	11:AL:366:ASP:HB2	1.93	0.50
11:AN:331:LYS:O	11:AN:331:LYS:HD3	2.12	0.50
7:U:61:LYS:NZ	7:U:97:ARG:HG3	2.26	0.50
4:q:87:ARG:HH21	4:q:104:ASP:HB2	1.77	0.50
11:AC:152:LYS:O	11:AC:156:ASP:HB2	2.11	0.50
11:AC:159:TYR:HD1	11:AC:160:ALA:N	2.09	0.50
11:AL:391:VAL:HG12	11:AM:401:MET:HE2	1.94	0.50
11:AL:436:ARG:HG3	11:AL:478:ARG:HD2	1.93	0.50
11:AM:345:ARG:HG2	11:AM:350:LEU:HD12	1.94	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:O:85:TYR:HA	2:O:116:THR:O	2.12	0.50
1:W:297:PHE:CE1	2:Y:138:ASN:HA	2.47	0.50
5:b:88:LYS:HB3	5:b:106:THR:HG23	1.94	0.50
2:i:77:LEU:HA	2:i:122:PRO:HD3	1.92	0.50
7:t:85:ILE:HG13	7:t:105:VAL:HG12	1.94	0.50
11:AE:461:SER:HG	11:AE:486:TRP:CD1	2.29	0.50
11:AH:230:LEU:HD12	11:AI:230:LEU:HB3	1.94	0.50
11:AI:323:THR:HG22	11:AI:328:VAL:HG21	1.93	0.50
11:AO:401:MET:HE1	11:AP:401:MET:HE1	1.94	0.50
1:O:158:TYR:HB3	1:O:231:LEU:HD11	1.94	0.50
2:1:70:ILE:HG12	1:g:74:PRO:HG2	1.92	0.50
2:1:73:ARG:HB2	2:1:134:LYS:HG2	1.92	0.50
1:M:132:LEU:HB3	1:M:241:ILE:HG23	1.93	0.50
2:O:109:TRP:HB2	11:AF:36:LEU:HD11	1.93	0.50
1:o:120:MET:HG3	1:o:129:PHE:HB2	1.93	0.50
1:u:363:PHE:CZ	2:v:162:LEU:HD11	2.47	0.50
2:v:107:ALA:HB1	2:v:108:PRO:HD2	1.94	0.50
11:AE:483:TRP:CD1	11:AF:462:ILE:HG23	2.47	0.50
11:AB:320:MET:HG3	11:AD:320:MET:HG2	1.94	0.50
3:A:32:ASN:ND2	9:d:38:GLN:HG2	2.27	0.50
1:M:434:ILE:HB	1:M:437:ARG:HB2	1.93	0.50
1:N:389:ARG:HD3	1:N:390:PRO:HD2	1.93	0.50
5:R:39:ILE:HG13	10:6:695:GLN:HE22	1.77	0.50
7:U:114:LEU:H	7:U:114:LEU:HD12	1.77	0.50
1:f:165:ASP:O	1:f:167:ILE:HG12	2.12	0.50
1:h:106:GLU:HG2	1:h:237:ARG:HG2	1.94	0.50
1:u:205:SER:HB2	1:u:212:LEU:HD21	1.93	0.50
11:AO:241:ASN:HB3	11:AO:244:ALA:HB3	1.94	0.50
11:AR:127:HIS:CD2	11:AS:128:VAL:HG22	2.47	0.50
1:L:165:ASP:O	1:L:167:ILE:HG12	2.12	0.49
6:S:66:MET:HA	6:S:69:TYR:CD1	2.47	0.49
1:V:207:GLU:HB2	1:V:212:LEU:HD12	1.93	0.49
8:Z:32:VAL:HA	8:Z:41:VAL:HG12	1.93	0.49
1:h:54:VAL:HG21	2:v:36:LEU:HD12	1.94	0.49
11:AF:246:ARG:HB3	11:AF:251:LEU:HD12	1.93	0.49
11:AH:22:ASP:HB2	11:AH:44:PHE:CZ	2.48	0.49
11:AL:177:GLN:HB2	11:AL:180:HIS:CE1	2.46	0.49
11:AO:127:HIS:CE1	11:AP:128:VAL:HG22	2.47	0.49
2:1:110:TYR:HB3	11:AC:39:TYR:CD1	2.47	0.49
1:L:384:ARG:HH21	1:L:386:ASN:HD21	1.60	0.49
1:M:105:LEU:HB2	1:M:267:TRP:HE1	1.76	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:N:148:PHE:CZ	1:W:253:GLN:HA	2.47	0.49
1:V:115:SER:HB2	1:V:131:LEU:HB2	1.94	0.49
7:n:63:ARG:HA	7:n:63:ARG:NH1	2.27	0.49
1:o:158:TYR:HE1	1:o:176:SER:HB3	1.76	0.49
2:p:117:GLY:O	2:p:118:ASN:HB2	2.11	0.49
6:y:77:ASN:HB2	6:y:110:ASN:HD21	1.78	0.49
9:T:8:TYR:CE2	9:T:25:ASN:HB2	2.46	0.49
11:AE:186:GLN:HG2	11:AE:190:LEU:HG	1.94	0.49
11:AB:403:PHE:CE1	11:AB:418:PRO:HD3	2.47	0.49
8:P:2:ARG:HG3	9:J:277:ASN:ND2	2.27	0.49
1:W:161:LYS:HG3	1:W:228:ALA:HB2	1.94	0.49
11:AE:40:GLN:H	11:AE:40:GLN:CD	2.20	0.49
11:AF:347:ASN:HB3	11:AG:336:ALA:HB2	1.94	0.49
11:AB:403:PHE:HE1	11:AB:418:PRO:HD3	1.76	0.49
11:AJ:333:ASP:HB3	11:AJ:336:ALA:HB3	1.93	0.49
11:AJ:410:ILE:HD12	11:AJ:411:SER:H	1.76	0.49
11:AK:263:LEU:HB3	11:AM:263:LEU:HD12	1.94	0.49
11:AM:203:ALA:HB3	11:AM:218:LYS:HG2	1.93	0.49
2:1:28:ILE:O	2:1:31:ARG:HG3	2.12	0.49
3:C:231:SER:HB2	6:c:87:LEU:HD13	1.94	0.49
3:F:23:ARG:H	3:F:23:ARG:HD3	1.76	0.49
1:N:393:VAL:HG23	1:N:475:ALA:HA	1.92	0.49
1:W:132:LEU:HB3	1:W:241:ILE:HG23	1.92	0.49
1:W:434:ILE:HB	1:W:437:ARG:HB2	1.94	0.49
1:f:303:ILE:HD12	1:f:303:ILE:H	1.77	0.49
11:AG:410:ILE:HD12	11:AG:411:SER:H	1.77	0.49
11:AB:308:LYS:HD3	11:AB:308:LYS:H	1.76	0.49
11:AH:461:SER:HG	11:AH:486:TRP:CD1	2.30	0.49
11:AI:177:GLN:HB2	11:AI:180:HIS:CE1	2.47	0.49
11:AI:279:ARG:HB3	11:AI:284:ILE:HB	1.94	0.49
11:AQ:279:ARG:HG2	11:AQ:284:ILE:HD12	1.93	0.49
11:AQ:483:TRP:CZ2	11:AS:483:TRP:HH2	2.31	0.49
2:1:210:GLN:HB2	2:1:239:THR:HG22	1.93	0.49
3:C:79:ILE:HG22	3:C:81:ASN:H	1.77	0.49
2:O:175:GLY:HA2	2:O:209:PHE:CZ	2.46	0.49
11:AL:246:ARG:HA	11:AL:249:LEU:HB2	1.93	0.49
11:AQ:236:LEU:HD21	11:AS:236:LEU:HD22	1.94	0.49
11:AR:230:LEU:HD23	11:AS:232:LYS:HE2	1.94	0.49
2:1:180:ASN:HD21	11:AB:36:LEU:HG	1.76	0.49
3:A:232:GLN:HB3	6:I:83:MET:HE1	1.95	0.49
3:B:207:LYS:C	3:B:210:LYS:HZ3	2.20	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:W:24:VAL:O	1:W:28:VAL:HG23	2.13	0.49
2:Y:110:TYR:CE1	11:AR:39:TYR:HB3	2.48	0.49
2:p:110:TYR:CE1	11:AL:39:TYR:HB3	2.48	0.49
1:u:165:ASP:O	1:u:167:ILE:HG12	2.13	0.49
11:AE:296:LEU:HD21	11:AF:298:SER:HA	1.95	0.49
11:AF:254:THR:HG23	11:AG:259:SER:HA	1.93	0.49
11:AG:13:ILE:O	11:AG:16:GLU:HG3	2.12	0.49
11:AB:343:THR:HG22	11:AB:347:ASN:HD21	1.78	0.49
11:AH:1:MET:HE2	11:AJ:58:GLN:HE21	1.78	0.49
11:AN:251:LEU:HD22	11:AP:251:LEU:HD21	1.95	0.49
11:AN:461:SER:HG	11:AN:486:TRP:HD1	1.58	0.49
11:AQ:441:LEU:HG	11:AQ:476:GLY:HA2	1.94	0.49
11:AR:169:VAL:O	11:AS:163:HIS:HA	2.13	0.49
1:M:437:ARG:NH2	1:f:443:MET:HE3	2.28	0.49
8:Z:231:HIS:HA	8:j:245:GLN:HE22	1.77	0.49
6:c:34:TRP:HE1	6:c:36:SER:HA	1.77	0.49
7:t:40:PHE:O	7:t:51:GLY:HA3	2.12	0.49
9:J:6:ARG:HH21	9:J:289:TRP:HB2	1.78	0.49
9:J:8:TYR:CE2	9:J:25:ASN:HB2	2.48	0.49
9:J:203:ASN:HA	9:J:274:ARG:NH1	2.27	0.49
9:T:223:ILE:HG13	9:T:250:CYS:HA	1.94	0.49
11:AI:218:LYS:HZ2	11:AI:218:LYS:HB3	1.78	0.49
11:AP:13:ILE:O	11:AP:16:GLU:HG3	2.12	0.49
11:AQ:258:PRO:HG2	11:AQ:261:THR:HG21	1.95	0.49
11:AQ:486:TRP:HE3	11:AQ:487:SER:H	1.60	0.49
3:D:34:ILE:HD12	3:D:43:HIS:CD2	2.45	0.49
1:M:109:ILE:HD11	1:M:139:PRO:HD3	1.95	0.49
2:Y:198:LYS:HA	2:Y:204:TYR:CZ	2.48	0.49
2:i:110:TYR:HB3	11:AO:39:TYR:HD2	1.78	0.49
11:AE:162:LYS:HB2	11:AG:159:TYR:HB3	1.95	0.49
11:AF:51:LEU:HD23	11:AG:7:PRO:HB3	1.94	0.49
11:AF:174:THR:HG23	11:AF:186:GLN:HE22	1.76	0.49
11:AI:127:HIS:CE1	11:AJ:128:VAL:HG22	2.48	0.49
11:AM:88:LEU:HD11	11:AM:108:ARG:HB3	1.95	0.49
11:AN:22:ASP:HB2	11:AN:44:PHE:CZ	2.47	0.49
11:AP:297:ARG:NH2	11:AP:300:GLN:HG3	2.28	0.49
11:AS:75:SER:HB2	11:AS:87:CYS:HB3	1.95	0.49
2:1:84:ASN:HA	2:1:91:THR:H	1.78	0.49
2:1:116:THR:HG21	1:u:410:ASN:OD1	2.13	0.49
2:1:144:PRO:O	2:1:148:ILE:HG12	2.12	0.49
2:1:198:LYS:HA	2:1:204:TYR:CZ	2.47	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:I:33:TYR:HE1	1:V:11:ILE:HD11	1.78	0.49
2:Y:73:ARG:HB2	2:Y:134:LYS:HG2	1.94	0.49
1:g:158:TYR:HE1	1:g:176:SER:HB2	1.78	0.49
11:AB:243:THR:HG22	11:AB:246:ARG:HH22	1.77	0.49
11:AN:380:ASN:HD21	11:AO:369:SER:HA	1.77	0.49
11:AQ:350:LEU:HD21	11:AR:350:LEU:HD13	1.94	0.49
11:AR:246:ARG:HA	11:AR:249:LEU:HB2	1.95	0.49
3:E:217:ARG:CD	3:E:218:ASP:H	2.26	0.49
2:O:87:GLY:C	2:O:109:TRP:HB3	2.38	0.49
4:Q:120:ILE:HD11	5:l:41:HIS:CE1	2.48	0.49
1:W:403:ASN:HA	1:W:407:MET:HE3	1.95	0.49
2:p:110:TYR:HB3	11:AL:39:TYR:CD1	2.48	0.49
2:p:213:ARG:HB3	2:p:237:ILE:HB	1.95	0.49
5:r:116:SER:H	5:r:124:ARG:HH12	1.61	0.49
2:v:108:PRO:HD3	11:AH:36:LEU:HD22	1.95	0.49
11:AE:255:ALA:HA	11:AG:254:THR:HB	1.95	0.49
11:AL:295:PHE:HE2	11:AM:295:PHE:HB2	1.77	0.49
11:AN:296:LEU:HB2	11:AO:296:LEU:HB2	1.95	0.49
3:E:217:ARG:HD2	3:E:218:ASP:H	1.77	0.48
1:L:160:LEU:HB3	1:L:172:ILE:HD12	1.94	0.48
2:O:215:PHE:HB3	2:O:238:LEU:HB3	1.94	0.48
1:X:31:ASP:HB2	2:i:31:ARG:HH22	1.78	0.48
11:AG:143:ALA:O	11:AG:147:LEU:HB2	2.13	0.48
11:AG:333:ASP:HB3	11:AG:336:ALA:HB3	1.94	0.48
11:AB:258:PRO:HG2	11:AB:261:THR:HG21	1.95	0.48
11:AC:413:GLY:HA3	11:AC:425:TRP:NE1	2.28	0.48
11:AI:239:LEU:HD22	11:AJ:235:ASN:HA	1.94	0.48
11:AP:427:THR:HA	11:AP:491:ASN:HA	1.95	0.48
11:AQ:169:VAL:HA	11:AS:173:ALA:HB3	1.95	0.48
2:l:138:ASN:HA	1:g:297:PHE:CE1	2.48	0.48
3:E:137:GLU:HB2	3:E:184:LEU:HD11	1.95	0.48
3:F:61:ASP:HB2	4:q:48:THR:HG23	1.95	0.48
2:Y:110:TYR:HB3	11:AR:39:TYR:HD1	1.77	0.48
1:o:379:ARG:HH22	2:p:160:VAL:HG12	1.77	0.48
2:p:91:THR:HG22	2:p:92:GLU:H	1.78	0.48
1:u:303:ILE:H	1:u:303:ILE:HD12	1.78	0.48
4:w:43:ILE:HG23	4:w:44:ARG:HG3	1.96	0.48
11:AC:384:LYS:HG3	11:AD:390:ASP:HB2	1.94	0.48
11:AM:485:ASN:H	11:AM:485:ASN:HD22	1.60	0.48
11:AR:391:VAL:HG12	11:AS:401:MET:HE2	1.95	0.48
11:AR:392:TRP:HB3	11:AS:404:GLN:HG3	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:B:217:ARG:HD2	3:B:218:ASP:H	1.78	0.48
2:O:84:ASN:C	2:O:117:GLY:HA2	2.37	0.48
2:O:198:LYS:HA	2:O:204:TYR:CZ	2.48	0.48
1:W:28:VAL:HG12	2:Y:31:ARG:HH22	1.78	0.48
4:a:32:TRP:HZ3	4:a:132:TRP:HE1	1.61	0.48
1:g:158:TYR:HB3	1:g:231:LEU:HD21	1.95	0.48
2:i:93:ARG:HH11	2:i:93:ARG:HA	1.78	0.48
7:t:63:ARG:NH1	7:t:63:ARG:HA	2.28	0.48
7:z:114:LEU:HD12	7:z:114:LEU:H	1.78	0.48
11:AG:454:VAL:HG22	11:AG:467:PHE:HE2	1.78	0.48
11:AB:486:TRP:HB2	11:AB:488:TYR:CD2	2.48	0.48
11:AC:91:HIS:CE1	11:AC:94:LYS:HB2	2.49	0.48
11:AD:75:SER:HB2	11:AD:87:CYS:HB3	1.95	0.48
11:AH:255:ALA:HA	11:AJ:254:THR:HB	1.94	0.48
11:AJ:32:TRP:CH2	11:AJ:37:PRO:HB3	2.48	0.48
11:AL:158:ARG:NH2	11:AM:155:GLY:HA2	2.29	0.48
11:AP:410:ILE:HD12	11:AP:411:SER:H	1.77	0.48
2:1:88:PHE:CG	2:1:109:TRP:HB3	2.48	0.48
3:D:176:GLU:HB3	4:G:43:ILE:HD11	1.94	0.48
6:I:18:ARG:HH22	9:T:212:MET:HG3	1.78	0.48
2:O:67:ILE:O	2:O:71:VAL:HG22	2.13	0.48
1:W:109:ILE:HD11	1:W:139:PRO:HD3	1.95	0.48
1:W:143:SER:HB3	1:W:237:ARG:HG3	1.96	0.48
1:X:389:ARG:HD3	1:X:390:PRO:HD2	1.94	0.48
2:Y:144:PRO:O	2:Y:148:ILE:HG12	2.13	0.48
2:i:175:GLY:HA2	2:i:209:PHE:CZ	2.48	0.48
1:o:363:PHE:HZ	2:p:170:VAL:HG21	1.79	0.48
9:d:293:CYS:C	9:d:294:TRP:HD1	2.21	0.48
11:AE:380:ASN:HD21	11:AF:369:SER:HA	1.78	0.48
11:AC:253:ASP:O	11:AC:257:MET:HG3	2.13	0.48
11:AK:467:PHE:CE1	11:AK:488:TYR:HB3	2.49	0.48
11:AL:23:PRO:HG3	11:AL:41:THR:HG23	1.95	0.48
11:AO:58:GLN:HG2	11:AO:59:HIS:HD2	1.77	0.48
11:AR:433:ASP:HB2	11:AR:484:GLY:H	1.78	0.48
3:F:60:ALA:HB1	4:q:49:ARG:HH21	1.78	0.48
4:G:115:THR:HB	4:G:121:GLU:CD	2.37	0.48
1:L:158:TYR:HB2	1:L:174:TYR:O	2.14	0.48
1:M:437:ARG:NH1	1:f:446:PRO:HA	2.29	0.48
8:P:179:ILE:HD13	8:j:171:ILE:HB	1.94	0.48
5:l:15:ALA:HA	5:l:90:PRO:HG2	1.95	0.48
1:o:372:GLU:HG2	1:o:384:ARG:HD3	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:p:144:PRO:O	2:p:148:ILE:HG12	2.14	0.48
7:t:63:ARG:HA	7:t:63:ARG:HH11	1.78	0.48
11:AB:246:ARG:HG2	11:AB:251:LEU:HD12	1.96	0.48
11:AC:169:VAL:O	11:AD:163:HIS:HA	2.13	0.48
11:AD:325:PRO:O	11:AD:328:VAL:HG22	2.13	0.48
11:AH:1:MET:HB2	11:AI:69:GLU:HB3	1.95	0.48
11:AJ:91:HIS:CE1	11:AJ:94:LYS:HB2	2.48	0.48
11:AO:323:THR:HG22	11:AO:328:VAL:HG21	1.94	0.48
11:AQ:51:LEU:HG	11:AR:7:PRO:HD3	1.96	0.48
2:1:91:THR:HG22	2:1:92:GLU:H	1.78	0.48
8:P:60:PRO:HD2	8:P:118:MET:HE1	1.94	0.48
1:V:146:GLY:HA2	1:V:213:PHE:HA	1.94	0.48
1:V:343:PRO:HG2	1:V:387:TYR:HB2	1.95	0.48
2:Y:165:TYR:HD2	2:Y:171:ARG:HD3	1.78	0.48
8:j:98:VAL:HB	8:j:108:HIS:CE1	2.49	0.48
11:AF:469:THR:HG22	11:AF:479:VAL:HG22	1.95	0.48
11:AL:316:GLY:HA3	11:AM:312:ARG:HH22	1.78	0.48
11:AO:335:LEU:HD22	11:AP:335:LEU:HD21	1.95	0.48
11:AP:471:MET:HE3	11:AP:478:ARG:HH21	1.79	0.48
2:1:85:TYR:HA	2:1:117:GLY:N	2.29	0.48
3:B:24:GLN:NE2	3:B:26:ARG:HD3	2.29	0.48
5:H:15:ALA:HB2	5:H:89:PHE:HB2	1.95	0.48
4:Q:115:THR:HG23	4:a:29:GLU:HG2	1.96	0.48
1:W:29:PHE:HA	2:Y:31:ARG:NH2	2.29	0.48
2:Y:80:GLN:HE22	2:Y:118:ASN:HA	1.78	0.48
1:f:160:LEU:HB3	1:f:172:ILE:O	2.13	0.48
1:g:397:ILE:HG12	1:g:455:ILE:HG22	1.96	0.48
2:i:84:ASN:HA	2:i:91:THR:N	2.19	0.48
4:w:79:GLN:H	4:w:79:GLN:HG2	1.51	0.48
9:T:3:GLN:HB3	9:T:84:TYR:CE2	2.48	0.48
11:AB:236:LEU:HD21	11:AD:236:LEU:HD22	1.95	0.48
11:AD:417:LEU:HB2	11:AD:421:LEU:HB2	1.96	0.48
11:AH:165:ASN:N	11:AJ:171:SER:HB2	2.28	0.48
11:AN:339:ALA:N	11:AO:334:ASN:HD21	2.08	0.48
3:A:53:LEU:HD23	3:A:188:MET:HE2	1.96	0.48
3:B:100:ARG:O	3:B:101:LEU:HB3	2.14	0.48
3:D:107:PHE:HD2	3:D:111:ILE:HG13	1.79	0.48
2:O:98:GLY:O	11:AE:38:PRO:HA	2.13	0.48
1:V:93:ARG:HB3	1:V:288:LEU:HD12	1.95	0.48
7:e:11:ASP:OD2	2:i:26:LYS:HB3	2.13	0.48
1:h:389:ARG:HD3	1:h:390:PRO:HD2	1.96	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:h:396:GLU:HA	1:h:481:ASP:HB3	1.95	0.48
11:AC:459:ASN:HD21	11:AC:461:SER:HB2	1.78	0.48
11:AI:441:LEU:HD11	11:AI:447:ILE:HD11	1.94	0.48
11:AK:58:GLN:HE22	11:AL:3:ASN:HA	1.78	0.48
11:AM:462:ILE:HG22	11:AM:485:ASN:ND2	2.29	0.48
11:AN:40:GLN:H	11:AN:40:GLN:CD	2.22	0.48
11:AP:205:ALA:O	11:AP:224:LYS:HG3	2.13	0.48
11:AR:209:GLU:OE1	11:AR:218:LYS:HG3	2.14	0.48
11:AS:88:LEU:HD11	11:AS:108:ARG:HB3	1.95	0.48
1:f:159:GLU:HB3	1:f:228:ALA:HB2	1.96	0.48
1:f:399:ILE:HB	1:f:484:VAL:HG13	1.95	0.48
2:i:67:ILE:O	2:i:71:VAL:HG22	2.13	0.48
6:m:66:MET:HA	6:m:69:TYR:CD1	2.49	0.48
9:d:226:PRO:HB2	9:d:269:LEU:HD12	1.95	0.48
11:AG:471:MET:HE3	11:AG:478:ARG:HH21	1.79	0.48
11:AB:455:MET:SD	11:AB:489:PRO:HB2	2.54	0.48
11:AC:230:LEU:HD23	11:AD:232:LYS:HE2	1.95	0.48
11:AK:144:ARG:HA	11:AK:147:LEU:HB2	1.95	0.48
11:AL:127:HIS:CD2	11:AM:128:VAL:HG22	2.48	0.48
1:0:422:TYR:CD2	1:0:441:PRO:HG3	2.48	0.48
3:A:29:VAL:HG13	3:A:44:ILE:HG23	1.96	0.48
3:F:100:ARG:O	3:F:101:LEU:HB3	2.13	0.48
1:M:163:TYR:CE1	1:M:169:THR:HG22	2.49	0.48
1:V:310:GLY:O	1:V:314:VAL:HG23	2.14	0.48
2:v:91:THR:HG22	2:v:92:GLU:H	1.78	0.48
9:T:10:LEU:HD23	9:T:23:ILE:HD12	1.96	0.48
11:AE:108:ARG:HH21	11:AF:113:ASP:CG	2.22	0.48
11:AH:40:GLN:H	11:AH:40:GLN:CD	2.20	0.48
11:AH:292:GLU:HB2	11:AH:297:ARG:HD3	1.95	0.48
11:AJ:13:ILE:O	11:AJ:16:GLU:HG3	2.14	0.48
11:AK:96:PRO:HG3	11:AK:107:TRP:CE2	2.48	0.48
11:AK:454:VAL:HG22	11:AK:467:PHE:CE2	2.48	0.48
11:AL:320:MET:HB3	11:AM:325:PRO:HB3	1.96	0.48
11:AS:436:ARG:HG3	11:AS:478:ARG:HH11	1.79	0.48
1:M:27:GLN:CD	11:AM:2:PRO:HB3	2.39	0.47
1:N:54:VAL:HG21	2:O:36:LEU:HD12	1.96	0.47
6:m:54:LEU:HD11	6:m:71:MET:HE3	1.95	0.47
7:n:114:LEU:H	7:n:114:LEU:HD12	1.79	0.47
2:p:61:GLY:H	2:p:64:LEU:HD12	1.78	0.47
11:AC:316:GLY:HA3	11:AD:312:ARG:HH12	1.79	0.47
11:AH:171:SER:H	11:AI:164:GLY:HA3	1.79	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:AK:483:TRP:CD2	11:AL:462:ILE:HA	2.49	0.47
11:AL:242:VAL:HG12	11:AL:246:ARG:HH11	1.79	0.47
11:AN:32:TRP:CH2	11:AN:37:PRO:HB3	2.49	0.47
3:C:233:ASP:CG	3:C:235:PRO:HD2	2.38	0.47
2:O:108:PRO:HB3	11:AE:37:PRO:HD3	1.95	0.47
2:Y:215:PHE:HD2	2:Y:242:VAL:HG11	1.79	0.47
1:f:363:PHE:CZ	2:i:162:LEU:HD11	2.50	0.47
1:g:357:ILE:O	1:g:361:LYS:HB2	2.14	0.47
4:k:8:TYR:HD2	5:r:51:VAL:HG12	1.79	0.47
1:o:159:GLU:HB2	1:o:173:LYS:HE2	1.95	0.47
9:d:191:ASN:HD21	9:d:198:ASN:HB2	1.79	0.47
11:AD:202:MET:HG2	11:AD:219:ALA:HB2	1.95	0.47
11:AD:246:ARG:HG2	11:AD:251:LEU:HD12	1.95	0.47
11:AD:485:ASN:HD22	11:AD:485:ASN:H	1.62	0.47
11:AI:349:GLY:HA3	11:AJ:345:ARG:HH21	1.79	0.47
11:AK:88:LEU:HB2	11:AK:105:GLY:O	2.14	0.47
11:AK:177:GLN:HG3	11:AK:178:PRO:HD2	1.96	0.47
11:AL:317:LEU:HD13	11:AM:317:LEU:HD22	1.96	0.47
11:AM:162:LYS:HE3	11:AM:162:LYS:HB2	1.79	0.47
11:AM:401:MET:HE3	11:AM:403:PHE:HE1	1.80	0.47
3:C:64:LEU:HD11	4:a:87:ARG:HH11	1.78	0.47
3:E:210:LYS:NZ	6:S:21:VAL:HB	2.28	0.47
1:L:363:PHE:HZ	2:O:170:VAL:HG21	1.78	0.47
2:Y:186:LEU:HD23	2:Y:195:LEU:HD23	1.96	0.47
5:l:92:MET:HE2	5:l:103:LEU:HD12	1.96	0.47
7:n:1:MET:HE1	7:n:23:GLN:HA	1.97	0.47
2:p:198:LYS:HA	2:p:204:TYR:CZ	2.49	0.47
4:q:115:THR:HB	4:q:121:GLU:CD	2.39	0.47
7:z:92:ILE:HA	7:z:99:TYR:HB2	1.96	0.47
11:AB:151:SER:HB3	11:AB:154:GLU:HG3	1.95	0.47
11:AC:39:TYR:HD1	11:AC:39:TYR:H	1.62	0.47
11:AK:57:ASN:ND2	11:AM:68:THR:HG21	2.29	0.47
2:1:111:SER:O	2:1:114:ALA:HB2	2.15	0.47
5:H:69:PRO:HG3	5:R:141:VAL:HG11	1.95	0.47
7:K:63:ARG:HA	7:K:63:ARG:NH1	2.30	0.47
1:L:66:GLN:HE22	6:y:42:HIS:CD2	2.32	0.47
1:L:407:MET:HB2	1:L:448:PHE:HB3	1.95	0.47
1:M:46:ALA:HB2	7:n:19:ALA:HA	1.97	0.47
1:N:93:ARG:O	1:N:94:HIS:HB2	2.14	0.47
1:N:303:ILE:CG2	1:N:306:SER:H	2.28	0.47
7:U:44:TRP:NE1	7:U:46:LEU:HB2	2.29	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:W:172:ILE:HD13	1:W:195:VAL:HG22	1.97	0.47
11:AE:329:MET:HB3	11:AF:329:MET:HA	1.96	0.47
11:AB:180:HIS:HA	11:AC:170:PHE:O	2.14	0.47
11:AC:127:HIS:CD2	11:AD:128:VAL:HG22	2.49	0.47
11:AJ:471:MET:HE3	11:AJ:478:ARG:HH21	1.79	0.47
11:AK:308:LYS:O	11:AK:312:ARG:HG3	2.15	0.47
11:AL:434:ASP:HA	11:AM:458:PHE:CG	2.50	0.47
11:AM:55:HIS:HE1	11:AM:59:HIS:CD2	2.32	0.47
11:AO:246:ARG:HB3	11:AO:251:LEU:HD12	1.96	0.47
11:AR:392:TRP:O	11:AS:403:PHE:HB2	2.14	0.47
1:O:428:LYS:HG2	1:O:431:ASP:OD2	2.15	0.47
3:B:103:PRO:HD3	3:B:116:PRO:HG3	1.96	0.47
1:M:143:SER:HB3	1:M:237:ARG:HG3	1.96	0.47
1:M:161:LYS:HG3	1:M:228:ALA:HB2	1.96	0.47
2:O:137:LYS:HZ1	2:O:194:ALA:H	1.62	0.47
1:V:142:CYS:SG	1:V:145:VAL:HG13	2.54	0.47
1:W:296:LYS:HD2	2:Y:72:GLY:HA3	1.97	0.47
1:X:163:TYR:HB2	1:X:224:THR:HB	1.97	0.47
1:h:116:PRO:HG2	1:h:117:PRO:HD3	1.97	0.47
2:p:189:LEU:HD12	2:p:189:LEU:HA	1.75	0.47
7:t:61:LYS:NZ	7:t:97:ARG:HG3	2.28	0.47
7:t:101:MET:HE3	7:t:101:MET:HB3	1.72	0.47
11:AE:225:ALA:HB1	11:AG:229:TYR:HE2	1.79	0.47
11:AG:308:LYS:HB3	11:AG:312:ARG:HH12	1.79	0.47
11:AH:330:MET:SD	11:AJ:331:LYS:HB2	2.54	0.47
11:AK:479:VAL:HG21	11:AK:490:PHE:CZ	2.50	0.47
11:AO:320:MET:HG2	11:AP:323:THR:O	2.14	0.47
2:1:110:TYR:CE1	11:AC:39:TYR:HB3	2.49	0.47
2:1:240:ASN:HA	2:1:243:THR:HB	1.97	0.47
3:B:207:LYS:HA	9:d:69:ASN:OD1	2.15	0.47
6:I:73:HIS:CE1	6:I:74:ILE:HG12	2.50	0.47
1:M:32:LEU:HB2	2:p:31:ARG:HH21	1.78	0.47
1:M:74:PRO:HG2	2:p:70:ILE:HG12	1.96	0.47
1:V:428:LYS:HG2	1:V:431:ASP:OD2	2.15	0.47
1:W:429:ILE:HA	1:W:474:VAL:HB	1.96	0.47
7:e:63:ARG:HA	7:e:63:ARG:HH11	1.79	0.47
1:g:46:ALA:HB2	7:z:19:ALA:HA	1.96	0.47
1:g:121:ILE:HD13	1:g:128:VAL:HG12	1.97	0.47
1:h:342:LEU:HD11	1:h:388:GLN:HB3	1.96	0.47
2:i:88:PHE:HB2	2:i:95:GLY:N	2.28	0.47
2:p:165:TYR:HD2	2:p:171:ARG:HD3	1.80	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:t:39:THR:HG21	1:u:49:ARG:HH22	1.78	0.47
9:T:86:GLU:H	9:T:86:GLU:HG2	1.47	0.47
11:AH:186:GLN:HG2	11:AH:190:LEU:HG	1.95	0.47
11:AK:13:ILE:HB	11:AK:16:GLU:HB2	1.96	0.47
11:AO:318:THR:HB	11:AP:322:THR:O	2.15	0.47
11:AQ:254:THR:HB	11:AS:254:THR:HG21	1.95	0.47
1:0:120:MET:HG3	1:0:129:PHE:HB2	1.96	0.47
3:D:171:ASP:HB3	3:D:189:THR:HB	1.96	0.47
3:E:156:ARG:HE	4:a:44:ARG:NH2	2.13	0.47
1:L:446:PRO:HA	1:W:437:ARG:HH12	1.79	0.47
1:M:164:VAL:HG11	1:M:223:LYS:HE2	1.96	0.47
7:U:61:LYS:HD3	7:U:61:LYS:HA	1.58	0.47
1:X:412:GLU:H	1:X:412:GLU:CD	2.22	0.47
2:Y:109:TRP:CD1	2:Y:109:TRP:N	2.83	0.47
1:g:208:GLN:HE21	1:g:213:PHE:HE2	1.63	0.47
1:g:389:ARG:HD3	1:g:390:PRO:HD2	1.96	0.47
1:g:407:MET:HE2	1:g:407:MET:HB3	1.72	0.47
1:o:409:GLU:OE1	2:v:118:ASN:HB2	2.15	0.47
2:p:139:ARG:CZ	2:p:139:ARG:HA	2.44	0.47
4:q:5:VAL:HG21	5:r:108:TRP:CZ3	2.48	0.47
9:d:298:LEU:HD22	9:d:299:ASN:H	1.79	0.47
11:AH:288:ALA:HB2	11:AJ:288:ALA:HB2	1.96	0.47
11:AI:343:THR:HB	11:AJ:334:ASN:HD22	1.80	0.47
11:AK:292:GLU:HB2	11:AM:295:PHE:HE1	1.80	0.47
11:AK:434:ASP:HA	11:AL:458:PHE:HB2	1.95	0.47
11:AL:392:TRP:O	11:AM:403:PHE:HB2	2.14	0.47
11:AO:288:ALA:HB2	11:AP:288:ALA:HB1	1.96	0.47
11:AR:341:THR:HG22	11:AR:345:ARG:HH11	1.79	0.47
11:AS:144:ARG:HD2	11:AS:151:SER:HB3	1.95	0.47
3:B:44:ILE:HG12	3:D:168:ILE:HD12	1.96	0.47
3:C:230:THR:HB	1:o:290:GLU:OE1	2.15	0.47
3:F:57:VAL:HG11	3:F:136:ILE:HD12	1.96	0.47
1:N:116:PRO:HG2	1:N:117:PRO:HD3	1.97	0.47
2:i:86:PHE:HE2	2:i:110:TYR:H	1.63	0.47
2:i:97:PHE:HE1	11:AN:37:PRO:HG2	1.79	0.47
2:i:177:ILE:HB	2:i:210:GLN:HE21	1.80	0.47
9:J:47:SER:O	9:J:191:ASN:HB3	2.14	0.47
9:d:47:SER:O	9:d:191:ASN:HB3	2.14	0.47
11:AB:51:LEU:HG	11:AC:7:PRO:HD3	1.96	0.47
11:AB:387:ALA:HB1	11:AD:383:LEU:HD22	1.96	0.47
11:AB:403:PHE:HB3	11:AD:419:ASN:HB3	1.97	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:AK:142:ILE:HA	11:AK:145:GLN:HB2	1.97	0.47
11:AO:81:ASN:HD21	11:AO:83:ILE:HB	1.80	0.47
11:AO:255:ALA:HB2	11:AP:255:ALA:HA	1.96	0.47
11:AQ:331:LYS:HD2	11:AS:320:MET:HE1	1.96	0.47
1:O:292:PHE:C	1:O:294:ASN:H	2.22	0.47
1:O:303:ILE:H	1:O:303:ILE:HD12	1.79	0.47
1:N:300:ALA:H	2:O:139:ARG:HH12	1.62	0.47
2:O:126:GLU:HG3	2:O:181:VAL:HG13	1.95	0.47
7:e:63:ARG:HA	7:e:63:ARG:NH1	2.29	0.47
1:f:81:ALA:O	1:f:85:LEU:HB2	2.15	0.47
1:g:437:ARG:NH2	1:u:443:MET:HE3	2.28	0.47
1:h:437:ARG:HE	1:o:443:MET:HE3	1.80	0.47
8:j:144:HIS:CG	8:j:164:ARG:HH22	2.33	0.47
11:AE:151:SER:HA	11:AG:148:SER:O	2.15	0.47
11:AB:482:ASN:HB2	11:AC:458:PHE:HB2	1.97	0.47
11:AH:251:LEU:HD22	11:AJ:251:LEU:HD21	1.97	0.47
11:AQ:331:LYS:O	11:AQ:331:LYS:HD3	2.15	0.47
11:AR:158:ARG:HH22	11:AS:155:GLY:HA2	1.80	0.47
11:AR:255:ALA:HB2	11:AS:255:ALA:HA	1.96	0.47
2:O:209:PHE:HB2	2:O:239:THR:OG1	2.15	0.47
1:X:93:ARG:O	1:X:94:HIS:HB2	2.15	0.47
1:h:80:VAL:HG13	6:m:69:TYR:HE2	1.79	0.47
1:h:93:ARG:O	1:h:94:HIS:HB2	2.15	0.47
2:p:96:SER:O	2:p:106:GLY:HA3	2.15	0.47
9:T:234:THR:O	10:9:782:GLU:HB3	2.14	0.47
11:AF:315:LEU:HB3	11:AF:317:LEU:HD21	1.97	0.47
11:AG:55:HIS:CE1	11:AG:63:GLU:HB2	2.50	0.47
11:AH:108:ARG:HH21	11:AI:113:ASP:CG	2.23	0.47
11:AI:254:THR:HG23	11:AJ:259:SER:HA	1.97	0.47
11:AJ:205:ALA:O	11:AJ:224:LYS:HG3	2.15	0.47
11:AO:174:THR:HG23	11:AO:186:GLN:HE22	1.80	0.47
11:AR:450:VAL:HG13	11:AR:494:ALA:HB2	1.97	0.47
11:AS:162:LYS:HE3	11:AS:162:LYS:HB2	1.83	0.47
1:O:379:ARG:HH22	2:1:160:VAL:HG12	1.80	0.46
2:1:98:GLY:O	11:AB:38:PRO:HA	2.15	0.46
3:A:35:GLU:HG3	9:d:64:SER:HB3	1.96	0.46
7:K:1:MET:HE1	7:K:23:GLN:HA	1.97	0.46
1:V:86:VAL:HG21	1:V:288:LEU:HD21	1.97	0.46
6:c:47:ASP:HB3	6:c:53:ILE:HD11	1.97	0.46
1:f:188:LEU:HD22	1:f:212:LEU:HB3	1.97	0.46
2:i:134:LYS:NZ	2:i:138:ASN:HD22	2.11	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:t:44:TRP:NE1	7:t:46:LEU:HB2	2.30	0.46
1:u:104:VAL:HG22	1:u:239:LEU:HD23	1.97	0.46
2:v:27:PRO:O	2:v:31:ARG:HG3	2.15	0.46
11:AE:22:ASP:HB2	11:AE:44:PHE:CZ	2.50	0.46
11:AC:159:TYR:HA	11:AD:161:MET:N	2.30	0.46
11:AD:394:LEU:HD13	11:AD:395:PRO:HD2	1.97	0.46
11:AI:32:TRP:CH2	11:AI:37:PRO:HB3	2.50	0.46
2:1:186:LEU:HD23	2:1:195:LEU:HD23	1.97	0.46
3:B:228:ASN:ND2	3:B:229:ALA:H	2.13	0.46
3:F:156:ARG:HE	4:q:44:ARG:NH2	2.12	0.46
1:L:310:GLY:O	1:L:314:VAL:HG23	2.15	0.46
1:M:161:LYS:H	1:M:228:ALA:HB2	1.79	0.46
1:X:249:PRO:HA	1:X:279:GLY:H	1.80	0.46
1:X:299:GLN:O	1:X:301:THR:HG23	2.15	0.46
8:Z:148:ASP:HB3	8:Z:166:LYS:HA	1.97	0.46
2:i:209:PHE:HB2	2:i:239:THR:HG23	1.97	0.46
6:s:66:MET:HE1	6:s:76:PHE:HD1	1.80	0.46
2:v:110:TYR:CD1	11:AI:39:TYR:HB3	2.50	0.46
11:AF:328:VAL:HG13	11:AG:330:MET:HG3	1.97	0.46
11:AF:401:MET:HE1	11:AG:401:MET:HE1	1.96	0.46
11:AC:471:MET:HG3	11:AC:478:ARG:HH21	1.80	0.46
11:AK:150:TYR:CE2	11:AL:152:LYS:HA	2.49	0.46
11:AL:255:ALA:HB2	11:AM:255:ALA:O	2.16	0.46
1:0:103:VAL:HG12	1:0:272:ASN:HB3	1.97	0.46
3:B:131:LYS:HE2	3:B:131:LYS:HB2	1.76	0.46
6:c:48:GLU:HB3	9:J:155:ALA:HB2	1.96	0.46
1:g:109:ILE:HD11	1:g:139:PRO:HD3	1.97	0.46
1:g:120:MET:HE3	1:g:120:MET:HB2	1.77	0.46
1:o:103:VAL:HG12	1:o:272:ASN:HB3	1.97	0.46
1:o:292:PHE:C	1:o:294:ASN:H	2.22	0.46
1:o:342:LEU:HD21	1:o:388:GLN:HB3	1.97	0.46
2:p:110:TYR:HB3	11:AL:39:TYR:HD1	1.79	0.46
1:u:184:SER:HA	1:u:187:ILE:HD12	1.97	0.46
4:w:123:ARG:N	4:w:123:ARG:HD2	2.31	0.46
9:d:141:ILE:HD13	9:d:199:VAL:HG21	1.96	0.46
11:AI:431:LEU:HD12	11:AI:467:PHE:HE2	1.79	0.46
11:AK:210:THR:HG22	11:AK:228:VAL:HG21	1.96	0.46
11:AK:387:ALA:HB1	11:AM:383:LEU:HD22	1.97	0.46
11:AM:91:HIS:CE1	11:AM:94:LYS:HB2	2.50	0.46
11:AN:43:ASN:ND2	11:AP:32:TRP:H	2.13	0.46
11:AP:33:VAL:HG23	11:AP:35:GLU:OE1	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:B:24:GLN:HE21	3:B:26:ARG:HD3	1.81	0.46
1:M:439:TYR:HD2	1:f:439:TYR:CG	2.34	0.46
2:O:238:LEU:HD23	2:O:238:LEU:H	1.80	0.46
8:P:208:HIS:HA	8:j:202:TRP:HB3	1.97	0.46
1:V:422:TYR:CD2	1:V:441:PRO:HG3	2.50	0.46
7:e:61:LYS:NZ	7:e:97:ARG:HG3	2.31	0.46
1:o:142:CYS:SG	1:o:145:VAL:HG13	2.56	0.46
2:p:180:ASN:ND2	11:AK:36:LEU:HG	2.30	0.46
1:u:379:ARG:HE	2:v:159:GLU:HA	1.80	0.46
9:d:8:TYR:CG	9:d:39:PHE:HE1	2.34	0.46
10:8:758:GLN:O	10:8:762:ARG:HG3	2.16	0.46
11:AG:410:ILE:H	11:AG:410:ILE:HG13	1.44	0.46
11:AC:307:ASN:ND2	11:AC:309:ALA:HB3	2.30	0.46
11:AN:305:VAL:HG13	11:AO:301:ASN:HA	1.96	0.46
11:AP:205:ALA:HB1	11:AP:210:THR:OG1	2.15	0.46
11:AS:32:TRP:CH2	11:AS:37:PRO:HB3	2.50	0.46
1:0:437:ARG:NH1	1:N:447:GLY:H	2.14	0.46
2:1:165:TYR:HD2	2:1:171:ARG:HD3	1.80	0.46
3:A:226:ALA:H	1:V:296:LYS:CE	2.28	0.46
1:N:298:VAL:HB	2:O:139:ARG:CZ	2.45	0.46
8:P:98:VAL:HB	8:P:108:HIS:CE1	2.50	0.46
8:P:231:HIS:O	8:j:241:THR:HG23	2.15	0.46
1:V:103:VAL:HG12	1:V:272:ASN:HB3	1.97	0.46
1:V:363:PHE:HD1	2:Y:144:PRO:HG3	1.81	0.46
1:W:28:VAL:C	2:Y:31:ARG:HH22	2.24	0.46
1:X:298:VAL:HB	2:i:139:ARG:CZ	2.45	0.46
2:Y:111:SER:O	2:Y:114:ALA:HB2	2.14	0.46
6:c:65:ILE:HG23	6:c:80:PHE:HB2	1.97	0.46
1:o:208:GLN:HB3	1:o:213:PHE:HE1	1.79	0.46
7:z:63:ARG:HA	7:z:63:ARG:NH1	2.30	0.46
11:AE:70:TYR:HD2	11:AE:75:SER:HB3	1.80	0.46
11:AF:88:LEU:HD21	11:AF:108:ARG:HG2	1.98	0.46
11:AF:236:LEU:HD22	11:AG:236:LEU:HD11	1.98	0.46
11:AD:462:ILE:HG22	11:AD:485:ASN:ND2	2.30	0.46
11:AM:165:ASN:H	11:AM:168:ASN:ND2	2.13	0.46
11:AQ:144:ARG:HA	11:AQ:147:LEU:HB2	1.98	0.46
11:AQ:329:MET:HG3	11:AQ:330:MET:HG3	1.97	0.46
11:AR:199:ALA:HB2	11:AS:203:ALA:HB2	1.98	0.46
1:N:406:SER:HB3	1:N:447:GLY:HA2	1.97	0.46
2:O:85:TYR:HD2	2:O:116:THR:HA	1.80	0.46
1:V:292:PHE:C	1:V:294:ASN:H	2.24	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:X:5:THR:HG22	1:X:6:ALA:H	1.81	0.46
6:s:23:ILE:HD11	6:s:108:TYR:CZ	2.51	0.46
9:J:183:CYS:SG	9:J:190:TRP:HD1	2.39	0.46
11:AE:13:ILE:HB	11:AE:16:GLU:HB2	1.97	0.46
11:AE:317:LEU:HD13	11:AG:317:LEU:HD21	1.98	0.46
11:AB:186:GLN:HG2	11:AB:190:LEU:HG	1.98	0.46
11:AD:69:GLU:HG2	11:AD:91:HIS:O	2.16	0.46
11:AK:231:LYS:HZ2	11:AM:211:GLU:HA	1.81	0.46
11:AK:288:ALA:HA	11:AM:287:SER:HB2	1.97	0.46
11:AN:108:ARG:HH21	11:AO:113:ASP:CG	2.23	0.46
11:AN:222:PRO:HB3	11:AP:210:THR:HG23	1.96	0.46
11:AQ:57:ASN:ND2	11:AS:68:THR:HG21	2.31	0.46
11:AQ:339:ALA:HB2	11:AR:332:ALA:HA	1.98	0.46
11:AR:389:LEU:HD22	11:AS:400:ALA:HA	1.98	0.46
11:AS:394:LEU:HD13	11:AS:395:PRO:HD2	1.98	0.46
1:0:148:PHE:HA	1:0:188:LEU:HD21	1.97	0.46
1:L:363:PHE:CZ	2:O:162:LEU:HD11	2.51	0.46
2:p:186:LEU:HD23	2:p:195:LEU:HD23	1.98	0.46
4:q:55:LEU:HD23	4:q:55:LEU:HA	1.83	0.46
11:AF:279:ARG:HA	11:AF:284:ILE:HD12	1.98	0.46
11:AC:159:TYR:CD2	11:AD:158:ARG:HB2	2.51	0.46
11:AD:88:LEU:HD21	11:AD:108:ARG:HG2	1.98	0.46
11:AI:144:ARG:HH22	11:AI:149:VAL:H	1.63	0.46
1:0:321:ARG:HH21	1:0:323:ILE:HD11	1.81	0.46
3:F:210:LYS:NZ	6:m:21:VAL:HB	2.31	0.46
4:G:143:VAL:HA	5:H:86:MET:HE2	1.98	0.46
1:N:144:GLY:HA3	1:N:215:VAL:HG12	1.97	0.46
1:N:454:THR:OG1	1:N:462:GLN:HB3	2.16	0.46
7:U:2:ASP:HB3	7:U:31:GLN:HE22	1.81	0.46
1:V:104:VAL:HG22	1:V:239:LEU:HD23	1.97	0.46
1:h:412:GLU:H	1:h:412:GLU:CD	2.23	0.46
7:n:113:SER:OG	1:o:35:THR:HB	2.16	0.46
11:AE:279:ARG:HA	11:AE:284:ILE:HD12	1.97	0.46
11:AC:450:VAL:HG13	11:AC:494:ALA:HB2	1.98	0.46
11:AD:328:VAL:HG23	11:AD:330:MET:HG3	1.96	0.46
11:AI:32:TRP:H	11:AJ:43:ASN:HD21	1.64	0.46
11:AI:96:PRO:HB3	11:AI:107:TRP:CG	2.50	0.46
11:AI:447:ILE:HG12	11:AI:496:THR:HG22	1.97	0.46
11:AJ:315:LEU:HB3	11:AJ:317:LEU:HD13	1.98	0.46
11:AK:449:ASN:HD21	11:AL:491:ASN:HB2	1.81	0.46
11:AN:71:GLN:HA	11:AN:90:THR:HG22	1.96	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:AP:91:HIS:CE1	11:AP:94:LYS:HB2	2.50	0.46
11:AQ:57:ASN:HD21	11:AS:68:THR:HG21	1.80	0.46
1:0:203:LEU:HA	1:0:216:PRO:HA	1.97	0.46
3:B:204:ARG:CZ	6:y:17:TYR:HB3	2.45	0.46
3:D:147:ALA:HB3	9:d:34:ARG:HH12	1.80	0.46
3:F:82:LYS:HD3	3:F:82:LYS:HA	1.61	0.46
3:F:217:ARG:HD2	3:F:218:ASP:H	1.79	0.46
3:F:222:GLY:O	3:F:228:ASN:HB3	2.15	0.46
7:K:1:MET:HE3	1:V:34:SER:H	1.80	0.46
1:V:369:GLY:HA3	1:V:387:TYR:C	2.41	0.46
4:a:120:ILE:HG23	5:r:51:VAL:HG11	1.98	0.46
1:g:94:HIS:HB3	1:g:95:ALA:H	1.59	0.46
1:h:5:THR:HG22	1:h:6:ALA:H	1.80	0.46
1:o:122:SER:HB2	1:o:257:ILE:HG22	1.97	0.46
2:p:93:ARG:HA	2:p:93:ARG:NH1	2.31	0.46
7:t:61:LYS:HD3	7:t:61:LYS:HA	1.65	0.46
2:v:87:GLY:C	2:v:109:TRP:HB3	2.41	0.46
9:J:27:HIS:CE1	9:J:33:ASN:HB2	2.50	0.46
11:AE:288:ALA:HB2	11:AG:288:ALA:HB2	1.98	0.46
11:AK:320:MET:HE1	11:AL:329:MET:HB2	1.97	0.46
11:AO:441:LEU:HD11	11:AO:447:ILE:HD11	1.98	0.46
2:1:4:ASN:HB2	2:1:51:GLN:HE21	1.81	0.46
2:1:139:ARG:HA	2:1:139:ARG:CZ	2.45	0.46
7:K:92:ILE:HA	7:K:99:TYR:HB2	1.97	0.46
1:M:296:LYS:HD2	2:p:72:GLY:HA3	1.98	0.46
2:O:81:ASP:HB3	2:O:84:ASN:HB3	1.98	0.46
2:O:198:LYS:HG3	2:O:204:TYR:CE1	2.51	0.46
5:R:41:HIS:CE1	4:w:120:ILE:HD11	2.50	0.46
1:V:120:MET:HG3	1:V:129:PHE:HB2	1.98	0.46
1:X:116:PRO:HG2	1:X:117:PRO:HD3	1.98	0.46
2:Y:139:ARG:HA	2:Y:139:ARG:CZ	2.45	0.46
1:f:172:ILE:O	1:f:172:ILE:HG13	2.16	0.46
2:i:88:PHE:O	2:i:107:ALA:HB3	2.16	0.46
7:n:61:LYS:HA	7:n:61:LYS:HD3	1.69	0.46
7:t:61:LYS:HZ3	7:t:97:ARG:HG3	1.81	0.46
11:AE:134:LEU:HD11	11:AG:137:ILE:HD13	1.97	0.46
11:AE:307:ASN:HB3	11:AE:310:GLN:HB3	1.98	0.46
11:AE:339:ALA:H	11:AF:334:ASN:HD21	1.64	0.46
11:AF:96:PRO:HB3	11:AF:107:TRP:CD1	2.51	0.46
11:AI:282:LEU:HA	11:AJ:275:LYS:NZ	2.31	0.46
11:AN:151:SER:HA	11:AP:148:SER:O	2.16	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:AR:186:GLN:HG2	11:AR:190:LEU:HG	1.98	0.46
1:0:296:LYS:CE	3:D:226:ALA:H	2.25	0.45
1:0:409:GLU:OE1	2:O:118:ASN:HB2	2.14	0.45
1:M:389:ARG:HD3	1:M:390:PRO:HD2	1.98	0.45
1:W:121:ILE:HD13	1:W:128:VAL:HG12	1.98	0.45
2:Y:108:PRO:HD3	11:AQ:36:LEU:HA	1.97	0.45
2:Y:238:LEU:HD23	2:Y:238:LEU:H	1.80	0.45
1:f:73:ASN:HB3	1:f:76:ALA:HB3	1.98	0.45
1:g:437:ARG:HA	1:g:437:ARG:HE	1.81	0.45
2:v:86:PHE:HE2	2:v:110:TYR:H	1.60	0.45
11:AE:231:LYS:HD3	11:AG:229:TYR:HE1	1.82	0.45
11:AE:329:MET:HB3	11:AF:330:MET:N	2.32	0.45
11:AB:464:PRO:HB3	11:AB:488:TYR:CE2	2.51	0.45
11:AC:467:PHE:CD2	11:AC:481:CYS:HB2	2.51	0.45
11:AI:159:TYR:CD1	11:AJ:160:ALA:HB3	2.50	0.45
11:AL:232:LYS:HB3	11:AL:233:LYS:NZ	2.31	0.45
11:AO:88:LEU:HD21	11:AO:108:ARG:HG2	1.99	0.45
11:AQ:231:LYS:HZ2	11:AS:211:GLU:HA	1.80	0.45
2:1:109:TRP:CD1	2:1:109:TRP:N	2.84	0.45
1:M:298:VAL:HG23	1:M:299:GLN:HE21	1.80	0.45
1:V:303:ILE:HD12	1:V:303:ILE:H	1.82	0.45
1:h:45:SER:O	1:h:49:ARG:HB2	2.16	0.45
9:d:234:THR:O	10:AA:782:GLU:HB3	2.16	0.45
11:AI:55:HIS:CE1	11:AJ:6:LYS:HB2	2.51	0.45
11:AK:301:ASN:HB3	11:AM:314:ASN:HD22	1.81	0.45
11:AL:202:MET:SD	11:AM:202:MET:HB3	2.56	0.45
11:AM:32:TRP:CH2	11:AM:37:PRO:HB3	2.51	0.45
11:AM:345:ARG:HB3	11:AM:350:LEU:HB2	1.97	0.45
11:AP:293:THR:HA	11:AP:297:ARG:NH1	2.31	0.45
11:AQ:314:ASN:OD1	11:AR:301:ASN:HB3	2.16	0.45
11:AR:391:VAL:HG21	11:AR:394:LEU:HD12	1.98	0.45
11:AS:165:ASN:HB3	11:AS:168:ASN:OD1	2.16	0.45
3:E:207:LYS:HA	9:T:69:ASN:ND2	2.31	0.45
1:N:5:THR:HG22	1:N:6:ALA:H	1.82	0.45
1:V:158:TYR:HB3	1:V:231:LEU:HD11	1.99	0.45
1:X:290:GLU:HA	1:X:293:ARG:HH21	1.80	0.45
8:Z:6:LEU:H	8:Z:6:LEU:HD12	1.81	0.45
1:f:471:PHE:CE1	1:f:472:LYS:HG3	2.52	0.45
4:k:120:ILE:H	4:k:120:ILE:HG13	1.52	0.45
1:o:174:TYR:CZ	1:o:190:GLY:HA3	2.52	0.45
6:s:34:TRP:HE1	6:s:36:SER:HA	1.81	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:s:73:HIS:CE1	6:s:74:ILE:HG12	2.51	0.45
1:u:310:GLY:O	1:u:314:VAL:HG23	2.16	0.45
11:AG:33:VAL:HG23	11:AG:35:GLU:OE1	2.17	0.45
11:AJ:410:ILE:H	11:AJ:410:ILE:HG13	1.45	0.45
11:AK:75:SER:HB2	11:AK:87:CYS:HB3	1.99	0.45
11:AL:150:TYR:CE1	11:AM:152:LYS:HA	2.51	0.45
11:AL:348:LEU:HD21	11:AM:335:LEU:HD13	1.98	0.45
11:AN:87:CYS:HB2	11:AN:107:TRP:CZ3	2.52	0.45
11:AR:424:GLN:CD	11:AR:442:PRO:HD2	2.42	0.45
2:1:196:LEU:HD12	2:1:206:TYR:HE2	1.81	0.45
3:E:60:ALA:HB1	4:a:49:ARG:HE	1.80	0.45
1:L:153:GLY:HA3	1:L:156:LEU:HD12	1.98	0.45
1:L:168:ASN:HB3	1:L:170:THR:HG23	1.99	0.45
1:M:289:ARG:HH11	1:M:289:ARG:HB2	1.80	0.45
4:Q:64:LEU:HD23	4:Q:64:LEU:HA	1.76	0.45
2:Y:110:TYR:HB3	11:AR:39:TYR:CD1	2.51	0.45
4:a:117:THR:HG23	4:a:119:GLY:H	1.80	0.45
8:j:117:ASN:ND2	8:j:118:MET:H	2.15	0.45
2:v:112:VAL:HG22	11:AI:38:PRO:CB	2.47	0.45
11:AE:462:ILE:HG23	11:AG:483:TRP:CG	2.51	0.45
11:AJ:275:LYS:HD3	11:AJ:275:LYS:HA	1.64	0.45
11:AL:158:ARG:HH22	11:AM:155:GLY:HA2	1.80	0.45
11:AL:315:LEU:HD23	11:AM:311:ALA:HB1	1.99	0.45
11:AO:139:ASN:HB3	11:AO:142:ILE:HB	1.98	0.45
11:AR:318:THR:HB	11:AS:324:ASP:HA	1.98	0.45
11:AR:431:LEU:HD23	11:AR:431:LEU:HA	1.79	0.45
2:1:126:GLU:O	2:1:130:ILE:HG22	2.16	0.45
3:E:169:PHE:CE1	3:E:172:LEU:HD12	2.50	0.45
1:f:207:GLU:HA	1:f:212:LEU:HA	1.98	0.45
1:f:379:ARG:HE	2:i:159:GLU:HA	1.81	0.45
1:g:163:TYR:CZ	1:g:169:THR:HG22	2.52	0.45
1:h:172:ILE:HG12	1:h:195:VAL:HG22	1.99	0.45
1:h:263:PRO:HG2	9:d:166:MET:HE1	1.98	0.45
1:h:357:ILE:O	1:h:361:LYS:HG2	2.17	0.45
2:p:108:PRO:HB3	11:AK:35:GLU:O	2.15	0.45
1:u:188:LEU:HD13	1:u:212:LEU:HB2	1.97	0.45
2:v:93:ARG:NH1	2:v:93:ARG:HA	2.32	0.45
2:v:110:TYR:HB3	11:AI:39:TYR:HD2	1.82	0.45
9:d:8:TYR:CE2	9:d:25:ASN:HB2	2.51	0.45
11:AE:236:LEU:HD13	11:AF:236:LEU:HD11	1.98	0.45
11:AF:278:ALA:O	11:AF:282:LEU:HB2	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:AB:367:ASN:HD22	11:AD:371:LEU:HD22	1.80	0.45
11:AD:371:LEU:HD23	11:AD:371:LEU:HA	1.86	0.45
11:AK:330:MET:HB3	11:AM:330:MET:N	2.31	0.45
11:AM:88:LEU:HD21	11:AM:108:ARG:HG2	1.97	0.45
1:N:445:ILE:HD12	1:N:446:PRO:HD2	1.98	0.45
4:Q:74:PHE:CZ	4:a:136:THR:HA	2.52	0.45
1:W:458:LYS:NZ	1:W:459:GLY:H	2.14	0.45
8:Z:244:PRO:HD3	8:j:229:HIS:O	2.17	0.45
4:q:74:PHE:CZ	4:w:136:THR:HA	2.51	0.45
9:T:6:ARG:HH21	9:T:289:TRP:HB2	1.81	0.45
11:AF:297:ARG:HB3	11:AF:297:ARG:HH11	1.82	0.45
11:AI:297:ARG:HB3	11:AI:297:ARG:HH11	1.82	0.45
11:AQ:295:PHE:HD1	11:AQ:295:PHE:HA	1.68	0.45
3:F:204:ARG:HD3	6:m:16:LYS:O	2.17	0.45
7:K:38:TYR:HB3	2:Y:22:GLN:HG2	1.98	0.45
1:M:458:LYS:NZ	1:M:459:GLY:H	2.15	0.45
8:P:9:LEU:HD12	10:8:773:ILE:HG13	1.99	0.45
1:W:73:ASN:HB2	2:Y:66:ILE:HD13	1.99	0.45
1:W:164:VAL:HG11	1:W:223:LYS:HE2	1.98	0.45
2:Y:110:TYR:CD1	11:AR:39:TYR:HB3	2.52	0.45
1:g:143:SER:HB3	1:g:237:ARG:HG3	1.99	0.45
1:h:296:LYS:HZ2	2:v:72:GLY:HA3	1.82	0.45
1:h:401:VAL:HG23	1:h:450:VAL:HA	1.99	0.45
1:o:88:PHE:HE1	2:p:56:LEU:HB2	1.82	0.45
2:p:238:LEU:HD23	2:p:238:LEU:H	1.80	0.45
11:AK:1:MET:HB2	11:AL:69:GLU:HB3	1.99	0.45
11:AL:159:TYR:HA	11:AM:161:MET:N	2.32	0.45
11:AN:186:GLN:HG2	11:AN:190:LEU:HG	1.98	0.45
11:AR:457:THR:HG22	11:AR:458:PHE:H	1.81	0.45
3:A:226:ALA:H	1:V:296:LYS:HE3	1.80	0.45
3:C:35:GLU:HG3	9:T:64:SER:HB3	1.98	0.45
3:D:127:GLN:HB3	3:D:128:LYS:H	1.59	0.45
3:D:233:ASP:CG	3:D:235:PRO:HD2	2.41	0.45
3:E:6:LYS:O	3:E:150:PHE:HB2	2.17	0.45
1:M:407:MET:HE2	1:M:407:MET:HB3	1.61	0.45
2:O:84:ASN:HA	2:O:91:THR:N	2.32	0.45
1:V:228:ALA:H	1:V:231:LEU:HD12	1.82	0.45
1:X:357:ILE:O	1:X:361:LYS:HG2	2.17	0.45
2:Y:91:THR:HG22	2:Y:92:GLU:H	1.81	0.45
8:Z:152:ALA:HB1	8:Z:155:LEU:HD21	1.98	0.45
1:h:11:ILE:HG21	1:h:66:GLN:HB2	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:i:126:GLU:HG3	2:i:181:VAL:HG13	1.99	0.45
2:p:101:SER:O	2:p:103:PRO:HD3	2.17	0.45
6:s:48:GLU:HB3	9:d:155:ALA:HB2	1.97	0.45
11:AE:441:LEU:HD11	11:AE:447:ILE:HD11	1.98	0.45
11:AD:432:SER:HB3	11:AD:487:SER:HB3	1.99	0.45
11:AJ:205:ALA:HB1	11:AJ:210:THR:OG1	2.16	0.45
11:AO:55:HIS:CE1	11:AP:6:LYS:HB2	2.52	0.45
11:AP:143:ALA:O	11:AP:147:LEU:HB2	2.16	0.45
11:AP:177:GLN:HB2	11:AP:180:HIS:CE1	2.52	0.45
11:AQ:228:VAL:O	11:AR:232:LYS:HB2	2.17	0.45
11:AQ:483:TRP:CD2	11:AR:462:ILE:HG12	2.51	0.45
1:M:73:ASN:ND2	1:M:75:ALA:HB3	2.31	0.45
1:M:129:PHE:CE1	1:M:244:ASP:HB2	2.52	0.45
8:Z:231:HIS:CE1	8:j:244:PRO:HG3	2.51	0.45
1:g:437:ARG:NH1	1:u:446:PRO:HA	2.31	0.45
7:z:44:TRP:NE1	7:z:46:LEU:HB3	2.32	0.45
9:d:6:ARG:HH21	9:d:289:TRP:HB2	1.82	0.45
11:AD:55:HIS:HE1	11:AD:59:HIS:CD2	2.34	0.45
11:AJ:33:VAL:HG23	11:AJ:35:GLU:OE1	2.17	0.45
11:AK:236:LEU:HD11	11:AM:236:LEU:HD13	1.99	0.45
11:AN:72:GLY:H	11:AN:90:THR:HG22	1.82	0.45
11:AN:171:SER:H	11:AO:164:GLY:HA3	1.82	0.45
11:AN:327:ALA:HA	11:AO:331:LYS:HB2	1.97	0.45
11:AP:55:HIS:CE1	11:AP:63:GLU:HB2	2.52	0.45
3:C:171:ASP:HB3	3:C:189:THR:HB	1.97	0.45
3:E:204:ARG:CZ	6:S:17:TYR:HB3	2.47	0.45
3:E:207:LYS:HA	9:T:69:ASN:HD21	1.80	0.45
7:K:19:ALA:HA	1:W:46:ALA:HB2	1.99	0.45
1:M:407:MET:HE2	1:M:448:PHE:HB3	1.99	0.45
2:O:26:LYS:HB3	7:U:11:ASP:OD2	2.16	0.45
4:Q:143:VAL:HA	5:R:86:MET:HE2	1.99	0.45
1:V:159:GLU:HB2	1:V:173:LYS:HE2	1.99	0.45
1:V:325:ASN:HD22	1:V:327:THR:H	1.65	0.45
1:V:409:GLU:OE1	2:i:118:ASN:HB2	2.17	0.45
1:W:132:LEU:HG	1:W:133:GLN:HG3	1.98	0.45
6:c:46:PHE:HD2	6:c:52:PRO:HA	1.82	0.45
1:o:158:TYR:HB3	1:o:231:LEU:HD11	1.98	0.45
1:o:397:ILE:HG13	1:o:482:ILE:HG12	1.97	0.45
6:s:18:ARG:HH22	9:d:212:MET:HG3	1.81	0.45
11:AG:131:TYR:O	11:AG:134:LEU:HD22	2.17	0.45
11:AC:91:HIS:CD2	11:AC:106:TYR:HD2	2.34	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:AC:246:ARG:HA	11:AC:249:LEU:HD12	1.99	0.45
11:AQ:88:LEU:HB2	11:AQ:105:GLY:O	2.17	0.45
11:AS:88:LEU:HD21	11:AS:108:ARG:HG2	1.99	0.45
1:0:363:PHE:HD1	2:1:144:PRO:HG3	1.82	0.44
3:A:127:GLN:HB3	3:A:128:LYS:H	1.56	0.44
3:D:174:PHE:N	3:D:174:PHE:CD1	2.85	0.44
3:E:204:ARG:HD3	6:S:16:LYS:O	2.17	0.44
1:L:439:TYR:O	1:L:443:MET:HG2	2.17	0.44
1:W:298:VAL:HG23	1:W:299:GLN:HE21	1.83	0.44
1:o:104:VAL:HG22	1:o:239:LEU:HD23	1.99	0.44
2:v:176:LYS:NZ	2:v:177:ILE:HG22	2.33	0.44
4:w:151:VAL:HG13	4:w:154:ALA:HB2	1.98	0.44
11:AE:195:THR:HG23	11:AE:197:THR:H	1.81	0.44
11:AE:312:ARG:HG2	11:AE:317:LEU:HD12	1.98	0.44
11:AB:468:MET:HE3	11:AB:481:CYS:HB2	1.99	0.44
11:AC:448:LEU:HD11	11:AC:497:SER:HB2	1.98	0.44
11:AH:257:MET:SD	11:AH:258:PRO:HD2	2.57	0.44
11:AH:451:GLN:NE2	11:AI:493:PHE:HB3	2.33	0.44
11:AK:467:PHE:O	11:AL:454:VAL:HB	2.17	0.44
11:AL:480:SER:OG	11:AM:457:THR:HA	2.17	0.44
3:F:6:LYS:O	3:F:150:PHE:HB2	2.16	0.44
4:G:34:SER:HB3	4:Q:41:ARG:HH22	1.82	0.44
4:G:108:VAL:HA	4:G:127:ILE:HD13	1.98	0.44
1:L:363:PHE:CZ	2:O:170:VAL:HG21	2.52	0.44
1:N:469:ILE:HG13	1:N:475:ALA:HB2	1.99	0.44
1:X:213:PHE:HD1	1:X:213:PHE:HA	1.72	0.44
6:c:43:MET:HE1	6:c:57:LEU:HD12	1.98	0.44
1:h:300:ALA:N	2:v:139:ARG:HH22	2.15	0.44
2:p:118:ASN:HB3	2:p:119:ALA:H	1.69	0.44
6:y:60:VAL:HG23	6:y:63:TYR:HB3	1.98	0.44
9:T:298:LEU:HD23	9:T:298:LEU:HA	1.77	0.44
11:AF:431:LEU:HD12	11:AF:467:PHE:HE2	1.82	0.44
11:AB:310:GLN:HE21	11:AB:314:ASN:HD21	1.65	0.44
11:AK:69:GLU:HG2	11:AK:92:SER:HB2	1.99	0.44
11:AK:406:ASN:HB2	11:AK:414:TRP:CZ2	2.52	0.44
11:AL:330:MET:HE2	11:AL:330:MET:HB3	1.92	0.44
11:AO:447:ILE:HG12	11:AO:496:THR:HG22	1.99	0.44
11:AS:447:ILE:HA	11:AS:496:THR:HG22	1.99	0.44
1:0:228:ALA:H	1:0:231:LEU:HD12	1.82	0.44
1:0:471:PHE:CZ	1:0:472:LYS:HE3	2.53	0.44
2:1:214:VAL:HA	2:1:239:THR:HG23	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:374:GLN:HG2	1:L:384:ARG:HG2	1.99	0.44
2:O:6:PHE:HD2	2:O:51:GLN:HG2	1.82	0.44
8:P:171:ILE:HB	8:Z:179:ILE:HG12	1.99	0.44
1:V:437:ARG:HG2	1:X:443:MET:SD	2.57	0.44
1:V:447:GLY:H	1:X:437:ARG:HH12	1.64	0.44
1:X:147:ILE:HD12	1:X:231:LEU:HD13	1.99	0.44
5:l:39:ILE:HG13	10:3:695:GLN:HE22	1.81	0.44
4:w:156:SER:O	4:w:159:ARG:HG3	2.18	0.44
9:T:245:GLY:HA2	9:T:296:SER:HA	2.00	0.44
11:AE:249:LEU:HD22	11:AF:249:LEU:HD11	1.98	0.44
11:AF:137:ILE:H	11:AF:137:ILE:HD12	1.82	0.44
11:AB:57:ASN:ND2	11:AD:68:THR:HG21	2.32	0.44
11:AB:236:LEU:HD11	11:AD:236:LEU:HD13	2.00	0.44
11:AB:368:LEU:HD22	11:AB:371:LEU:HD21	2.00	0.44
11:AC:436:ARG:HD2	11:AD:458:PHE:CE2	2.47	0.44
11:AD:122:ALA:HB1	11:AD:126:ARG:HH22	1.81	0.44
11:AH:13:ILE:HB	11:AH:16:GLU:HB2	1.99	0.44
11:AH:72:GLY:H	11:AH:90:THR:HG22	1.82	0.44
11:AK:434:ASP:HA	11:AL:458:PHE:CB	2.47	0.44
11:AM:328:VAL:HG23	11:AM:330:MET:N	2.32	0.44
11:AO:254:THR:HG23	11:AP:259:SER:HA	1.98	0.44
11:AP:231:LYS:HB3	11:AP:233:LYS:HE2	1.99	0.44
11:AQ:180:HIS:HA	11:AR:170:PHE:O	2.16	0.44
3:E:228:ASN:ND2	3:E:229:ALA:H	2.16	0.44
3:F:137:GLU:HB2	3:F:184:LEU:HD11	2.00	0.44
1:N:412:GLU:CD	1:N:412:GLU:H	2.24	0.44
2:i:33:LEU:HD23	2:i:33:LEU:HA	1.74	0.44
2:i:198:LYS:HG3	2:i:204:TYR:CE1	2.52	0.44
5:l:33:LYS:HG3	5:l:58:TRP:CE2	2.52	0.44
7:n:92:ILE:HA	7:n:99:TYR:HB2	1.99	0.44
2:v:177:ILE:HB	2:v:210:GLN:HG3	1.99	0.44
11:AG:406:ASN:HB3	11:AG:414:TRP:NE1	2.32	0.44
11:AB:13:ILE:HB	11:AB:16:GLU:HB2	2.00	0.44
11:AB:434:ASP:OD1	11:AC:458:PHE:HB2	2.16	0.44
11:AC:330:MET:HE2	11:AC:330:MET:HB3	1.92	0.44
11:AD:439:ILE:HD13	11:AD:439:ILE:HA	1.88	0.44
11:AK:222:PRO:HD3	11:AM:218:LYS:O	2.16	0.44
11:AO:328:VAL:HG13	11:AP:330:MET:HG3	1.99	0.44
11:AQ:142:ILE:HA	11:AQ:145:GLN:HB2	2.00	0.44
11:AQ:449:ASN:HD21	11:AR:491:ASN:HB2	1.81	0.44
11:AS:348:LEU:HD23	11:AS:348:LEU:HA	1.85	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:0:342:LEU:HD21	1:0:388:GLN:HB3	1.99	0.44
3:D:100:ARG:O	3:D:101:LEU:HB3	2.17	0.44
3:E:131:LYS:HE2	3:E:131:LYS:HB2	1.77	0.44
7:K:59:LEU:HD13	7:K:59:LEU:HA	1.83	0.44
1:N:11:ILE:HG21	1:N:66:GLN:HB2	2.00	0.44
1:N:469:ILE:HD13	1:N:469:ILE:HA	1.89	0.44
7:U:40:PHE:O	7:U:51:GLY:HA3	2.17	0.44
1:V:160:LEU:HD12	1:V:227:GLU:HA	2.00	0.44
1:X:302:ASN:OD1	1:f:303:ILE:HD11	2.18	0.44
4:a:120:ILE:H	4:a:120:ILE:HG13	1.56	0.44
1:g:109:ILE:HD12	1:g:109:ILE:HA	1.86	0.44
1:h:445:ILE:HD12	1:h:446:PRO:HD2	2.00	0.44
2:i:14:VAL:O	2:i:18:ARG:HG2	2.18	0.44
2:p:126:GLU:O	2:p:130:ILE:HG22	2.17	0.44
7:z:44:TRP:HE1	7:z:46:LEU:HB3	1.82	0.44
9:J:298:LEU:HA	9:J:298:LEU:HD23	1.74	0.44
9:T:66:ALA:O	9:T:70:ILE:HG22	2.17	0.44
11:AF:159:TYR:CD2	11:AG:160:ALA:HB3	2.52	0.44
11:AF:175:ALA:HB2	11:AF:181:ALA:O	2.18	0.44
11:AB:329:MET:C	11:AB:331:LYS:H	2.26	0.44
11:AK:58:GLN:NE2	11:AL:3:ASN:HA	2.32	0.44
11:AL:317:LEU:HD21	11:AM:312:ARG:HG3	2.00	0.44
11:AM:122:ALA:HB1	11:AM:126:ARG:HH22	1.82	0.44
11:AO:446:ARG:HG2	11:AO:497:SER:O	2.18	0.44
1:0:162:MET:HE2	1:0:162:MET:HB3	1.86	0.44
3:B:169:PHE:CE1	3:B:172:LEU:HD12	2.52	0.44
7:K:113:SER:OG	1:V:35:THR:HB	2.18	0.44
2:O:109:TRP:CD1	2:O:109:TRP:O	2.71	0.44
8:P:5:GLY:HA3	10:8:773:ILE:HG21	2.00	0.44
2:Y:93:ARG:NH1	2:Y:93:ARG:HA	2.33	0.44
1:g:49:ARG:O	1:g:53:VAL:HG23	2.18	0.44
1:g:300:ALA:HB1	1:g:306:SER:CB	2.46	0.44
1:g:439:TYR:HD2	1:u:439:TYR:CG	2.36	0.44
1:h:12:LYS:HE2	1:h:62:TRP:CZ2	2.52	0.44
8:j:4:THR:HG21	9:T:52:SER:HB3	1.99	0.44
4:k:156:SER:O	4:k:159:ARG:HG3	2.18	0.44
1:o:322:ILE:HD13	1:o:343:PRO:HA	2.00	0.44
5:r:38:PHE:HD1	5:r:50:ARG:HD2	1.83	0.44
9:J:3:GLN:HB3	9:J:84:TYR:CE2	2.52	0.44
9:J:61:TYR:CE1	9:J:110:VAL:HG22	2.52	0.44
9:J:300:GLN:H	9:J:300:GLN:HG3	1.55	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:AG:260:SER:HB3	11:AG:264:LYS:HE3	1.99	0.44
11:AD:32:TRP:CH2	11:AD:37:PRO:HB3	2.52	0.44
11:AK:384:LYS:HB3	11:AL:390:ASP:OD1	2.18	0.44
11:AK:404:GLN:O	11:AK:416:ARG:HB3	2.16	0.44
11:AK:482:ASN:HB2	11:AL:458:PHE:HB2	2.00	0.44
11:AN:257:MET:SD	11:AN:258:PRO:HD2	2.58	0.44
11:AO:417:LEU:HD23	11:AO:417:LEU:HA	1.83	0.44
11:AQ:159:TYR:HB3	11:AS:158:ARG:HG3	1.99	0.44
11:AR:23:PRO:HG3	11:AR:41:THR:HG23	1.99	0.44
11:AS:410:ILE:H	11:AS:410:ILE:HG13	1.49	0.44
1:O:183:THR:HG22	1:O:185:GLU:H	1.81	0.44
3:E:57:VAL:HG11	3:E:136:ILE:HD12	1.98	0.44
7:K:44:TRP:NE1	7:K:46:LEU:HB3	2.33	0.44
1:L:108:ASN:OD1	1:L:266:GLY:HA2	2.18	0.44
1:L:363:PHE:CE1	2:O:162:LEU:HD21	2.52	0.44
5:R:1:MET:HE2	5:R:1:MET:HB2	1.86	0.44
2:Y:101:SER:O	2:Y:103:PRO:HD3	2.17	0.44
6:c:13:GLN:HE22	6:c:98:ASP:HA	1.83	0.44
1:h:104:VAL:HG12	1:h:239:LEU:HD23	2.00	0.44
8:j:66:PRO:HD3	8:j:100:LYS:HE3	1.99	0.44
6:m:45:ILE:HG22	6:m:53:ILE:HD12	2.00	0.44
7:n:44:TRP:NE1	7:n:46:LEU:HB3	2.32	0.44
4:q:26:VAL:HG12	4:q:62:GLU:O	2.18	0.44
4:q:34:SER:HB3	4:w:41:ARG:HH22	1.83	0.44
1:u:379:ARG:HH12	2:v:148:ILE:HD12	1.83	0.44
9:d:278:VAL:HA	9:d:292:GLU:O	2.18	0.44
11:AB:263:LEU:HB3	11:AD:263:LEU:HD12	2.00	0.44
11:AB:493:PHE:HB3	11:AD:451:GLN:NE2	2.33	0.44
11:AC:116:GLU:HA	11:AC:119:LYS:HZ3	1.82	0.44
11:AD:91:HIS:CE1	11:AD:94:LYS:HB2	2.52	0.44
11:AJ:233:LYS:H	11:AJ:233:LYS:NZ	2.16	0.44
11:AL:159:TYR:CZ	11:AM:160:ALA:HB3	2.52	0.44
11:AM:467:PHE:CE1	11:AM:481:CYS:HB2	2.52	0.44
11:AO:431:LEU:HD12	11:AO:467:PHE:HE2	1.82	0.44
11:AR:159:TYR:CZ	11:AS:160:ALA:HB3	2.53	0.44
11:AS:13:ILE:HB	11:AS:16:GLU:HG2	2.00	0.44
1:O:35:THR:HB	7:z:113:SER:OG	2.17	0.44
2:1:14:VAL:O	2:1:18:ARG:HG2	2.18	0.44
3:C:169:PHE:HE1	3:C:188:MET:HB3	1.82	0.44
3:D:57:VAL:HG23	3:D:184:LEU:HB3	2.00	0.44
4:G:73:PHE:HB3	4:G:125:TRP:CZ3	2.52	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:K:45:PHE:CD1	2:Y:18:ARG:HD2	2.53	0.44
1:N:342:LEU:HD13	1:N:368:VAL:HG23	1.99	0.44
8:P:231:HIS:HA	8:Z:245:GLN:HE22	1.83	0.44
1:X:159:GLU:OE2	1:X:228:ALA:HB1	2.17	0.44
5:b:58:TRP:CG	5:b:133:VAL:HG21	2.53	0.44
1:g:458:LYS:NZ	1:g:459:GLY:H	2.14	0.44
1:h:359:LEU:HD12	1:h:359:LEU:HA	1.83	0.44
1:o:260:ILE:HD11	1:o:270:VAL:HG12	1.99	0.44
1:u:292:PHE:O	1:u:293:ARG:HB3	2.17	0.44
5:x:77:LEU:HD23	5:x:89:PHE:CE2	2.53	0.44
6:y:46:PHE:HD1	6:y:52:PRO:HA	1.82	0.44
11:AB:231:LYS:HD3	11:AD:229:TYR:HE1	1.83	0.44
11:AC:255:ALA:HB2	11:AD:255:ALA:O	2.17	0.44
11:AC:284:ILE:HG23	11:AD:288:ALA:HB1	1.99	0.44
11:AD:165:ASN:HB3	11:AD:168:ASN:OD1	2.18	0.44
11:AH:331:LYS:HE2	11:AJ:328:VAL:HA	2.00	0.44
11:AJ:422:LEU:HD22	11:AJ:424:GLN:HG2	2.00	0.44
11:AK:448:LEU:HB2	11:AK:495:ILE:O	2.18	0.44
11:AQ:75:SER:HB2	11:AQ:87:CYS:HB3	1.99	0.44
11:AR:308:LYS:HB2	11:AR:312:ARG:NH2	2.33	0.44
11:AR:312:ARG:HA	11:AR:317:LEU:HG	1.99	0.44
11:AS:55:HIS:HE1	11:AS:59:HIS:CD2	2.36	0.44
1:O:104:VAL:HG22	1:O:239:LEU:HD23	1.99	0.44
2:1:139:ARG:HH22	1:g:299:GLN:N	1.99	0.44
2:1:209:PHE:HB3	2:1:241:LEU:HB2	2.00	0.44
3:B:151:SER:HB3	3:B:164:ILE:O	2.18	0.44
3:F:33:PRO:HA	3:F:39:LYS:HD2	2.00	0.44
1:L:456:ALA:HB2	1:L:462:GLN:HA	1.99	0.44
1:M:248:GLY:HA2	1:M:281:LEU:HD21	1.99	0.44
6:S:17:TYR:N	6:S:17:TYR:CD1	2.86	0.44
1:V:290:GLU:O	1:V:294:ASN:HB2	2.18	0.44
1:V:298:VAL:HG23	1:V:299:GLN:H	1.83	0.44
1:g:361:LYS:HG2	1:g:362:PRO:O	2.18	0.44
1:o:422:TYR:CD2	1:o:441:PRO:HG3	2.52	0.44
5:r:136:ASN:ND2	5:r:165:GLY:HA3	2.33	0.44
11:AE:147:LEU:HD21	11:AF:134:LEU:HG	1.98	0.44
11:AE:215:ASN:HD21	11:AF:222:PRO:HB2	1.83	0.44
11:AH:483:TRP:CD1	11:AI:462:ILE:HG23	2.52	0.44
11:AJ:131:TYR:O	11:AJ:134:LEU:HD22	2.18	0.44
11:AK:180:HIS:HA	11:AL:170:PHE:O	2.18	0.44
11:AK:232:LYS:HD2	11:AM:238:GLY:C	2.43	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:AK:486:TRP:H	11:AK:488:TYR:HE1	1.66	0.44
11:AL:307:ASN:ND2	11:AL:309:ALA:HB3	2.33	0.44
11:AN:29:GLY:HA2	11:AO:16:GLU:OE1	2.18	0.44
11:AO:159:TYR:CD2	11:AP:160:ALA:HB3	2.53	0.44
11:AQ:288:ALA:HA	11:AS:287:SER:HB2	1.99	0.44
11:AQ:288:ALA:HB2	11:AR:288:ALA:HB1	1.99	0.44
11:AQ:307:ASN:HB3	11:AQ:310:GLN:HB3	2.00	0.44
11:AS:436:ARG:H	11:AS:436:ARG:HD2	1.83	0.44
2:1:72:GLY:HA3	1:g:296:LYS:HD2	2.00	0.43
3:A:234:SER:HB2	3:A:235:PRO:HD3	2.00	0.43
3:B:23:ARG:HD3	3:B:23:ARG:H	1.83	0.43
3:C:168:ILE:HD12	3:F:44:ILE:HG12	2.00	0.43
3:F:217:ARG:CD	3:F:218:ASP:H	2.31	0.43
1:N:296:LYS:HG3	2:O:72:GLY:HA3	2.00	0.43
4:a:74:PHE:CZ	4:k:136:THR:HA	2.53	0.43
7:e:44:TRP:CH2	1:f:49:ARG:HA	2.53	0.43
1:f:407:MET:HB2	1:f:448:PHE:HB3	2.00	0.43
1:g:403:ASN:HA	1:g:407:MET:HE1	2.00	0.43
1:h:159:GLU:OE2	1:h:228:ALA:HB1	2.18	0.43
1:h:443:MET:HE3	1:h:443:MET:HB2	1.79	0.43
2:i:174:ILE:HG21	2:i:178:LEU:HD21	2.00	0.43
8:j:104:THR:HG22	8:j:106:GLN:HG2	2.00	0.43
4:q:120:ILE:H	4:q:120:ILE:HG13	1.56	0.43
2:v:174:ILE:HB	2:v:208:GLU:HA	2.00	0.43
11:AE:251:LEU:HD22	11:AG:251:LEU:HD21	1.99	0.43
11:AG:328:VAL:HG23	11:AG:330:MET:HB2	1.99	0.43
11:AJ:454:VAL:HG22	11:AJ:467:PHE:HE2	1.83	0.43
11:AK:279:ARG:HG2	11:AK:284:ILE:HD12	2.00	0.43
11:AL:116:GLU:O	11:AL:120:VAL:HG23	2.18	0.43
11:AL:139:ASN:CG	11:AL:142:ILE:HB	2.43	0.43
11:AL:318:THR:HG22	11:AL:319:GLY:H	1.82	0.43
11:AN:13:ILE:HB	11:AN:16:GLU:HB2	1.99	0.43
11:AO:173:ALA:HB2	11:AP:166:GLY:O	2.18	0.43
11:AS:275:LYS:HD3	11:AS:275:LYS:H	1.83	0.43
2:1:100:LEU:HG	11:AB:40:GLN:HG3	2.00	0.43
2:1:224:GLN:HG3	2:1:236:GLY:HA2	2.01	0.43
3:C:234:SER:HB2	3:C:235:PRO:HD3	1.99	0.43
1:M:61:ILE:O	1:M:65:ILE:HG12	2.17	0.43
1:M:100:ARG:HE	1:M:241:ILE:HD11	1.83	0.43
1:M:162:MET:HG2	1:M:164:VAL:HG13	2.00	0.43
2:O:85:TYR:CD2	2:O:116:THR:HA	2.54	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:O:93:ARG:HG3	2:O:94:ALA:H	1.83	0.43
4:Q:99:THR:HA	4:Q:136:THR:O	2.18	0.43
7:U:69:ASP:O	7:U:73:GLN:HG2	2.19	0.43
1:V:379:ARG:HH22	2:Y:160:VAL:HG12	1.83	0.43
2:Y:92:GLU:H	2:Y:92:GLU:CD	2.25	0.43
8:Z:171:ILE:HB	8:j:179:ILE:HD13	2.00	0.43
7:e:12:LEU:HD11	2:i:29:PHE:HD2	1.83	0.43
7:n:38:TYR:HD1	7:n:38:TYR:HA	1.71	0.43
1:o:363:PHE:CZ	2:p:170:VAL:HG21	2.53	0.43
7:t:59:LEU:HD13	7:t:59:LEU:HA	1.92	0.43
2:v:198:LYS:HA	2:v:204:TYR:CZ	2.53	0.43
11:AD:462:ILE:HD12	11:AD:462:ILE:HA	1.82	0.43
11:AH:120:VAL:HG11	11:AJ:120:VAL:HG11	2.01	0.43
11:AI:150:TYR:CE1	11:AJ:152:LYS:HA	2.53	0.43
11:AK:186:GLN:HG2	11:AK:190:LEU:HG	2.00	0.43
11:AK:319:GLY:CA	11:AL:325:PRO:HG3	2.49	0.43
11:AL:417:LEU:HD23	11:AL:417:LEU:HA	1.88	0.43
11:AN:463:GLY:H	11:AP:483:TRP:CB	2.31	0.43
11:AO:23:PRO:HB2	11:AO:27:LYS:HB3	1.99	0.43
11:AR:13:ILE:HB	11:AR:16:GLU:OE2	2.18	0.43
11:AR:159:TYR:CD1	11:AR:160:ALA:N	2.85	0.43
3:B:131:LYS:CD	7:K:66:PRO:HB3	2.41	0.43
3:D:66:ARG:HH12	3:D:87:THR:HB	1.82	0.43
8:P:22:TYR:HB3	8:P:91:PHE:CD2	2.53	0.43
5:R:77:LEU:HD23	5:R:89:PHE:CE2	2.52	0.43
1:V:363:PHE:HZ	2:Y:170:VAL:HG21	1.83	0.43
4:a:79:GLN:H	4:a:79:GLN:HG2	1.56	0.43
1:g:449:GLN:HG3	1:u:434:ILE:HG21	1.99	0.43
2:i:136:ILE:HD13	2:i:136:ILE:HA	1.92	0.43
1:u:159:GLU:HB3	1:u:228:ALA:HB2	1.99	0.43
9:T:27:HIS:CE1	9:T:33:ASN:HD22	2.36	0.43
11:AE:462:ILE:HG23	11:AG:483:TRP:CD1	2.54	0.43
11:AB:286:SER:HA	11:AB:289:THR:HG23	2.00	0.43
11:AH:151:SER:HA	11:AJ:148:SER:O	2.18	0.43
11:AK:150:TYR:HE2	11:AL:152:LYS:HA	1.83	0.43
11:AN:329:MET:HB3	11:AO:330:MET:N	2.32	0.43
11:AP:401:MET:HE3	11:AP:403:PHE:HE1	1.84	0.43
11:AQ:331:LYS:HB2	11:AR:329:MET:HE2	2.00	0.43
11:AR:116:GLU:O	11:AR:120:VAL:HG23	2.18	0.43
3:B:164:ILE:H	3:B:164:ILE:HG13	1.64	0.43
3:B:188:MET:HE2	3:B:188:MET:HB3	1.93	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:F:207:LYS:HA	9:J:69:ASN:HD21	1.83	0.43
4:G:64:LEU:HD23	4:G:64:LEU:HA	1.80	0.43
7:K:61:LYS:HA	7:K:61:LYS:HD3	1.73	0.43
1:L:397:ILE:HA	1:L:455:ILE:HG22	2.00	0.43
1:M:223:LYS:HE2	1:M:223:LYS:HB3	1.80	0.43
1:N:263:PRO:HG2	9:T:166:MET:HE1	2.00	0.43
1:W:49:ARG:O	1:W:53:VAL:HG23	2.19	0.43
1:g:73:ASN:ND2	1:g:75:ALA:HB3	2.31	0.43
4:k:9:SER:HB2	4:k:12:ASP:OD2	2.18	0.43
6:m:17:TYR:N	6:m:17:TYR:HD1	2.17	0.43
7:n:39:THR:HG21	1:o:49:ARG:HH22	1.83	0.43
1:u:418:ARG:HE	1:u:418:ARG:HB2	1.61	0.43
4:w:76:LEU:HA	4:w:76:LEU:HD23	1.71	0.43
11:AG:455:MET:HG3	11:AG:489:PRO:HG2	2.01	0.43
11:AC:13:ILE:HB	11:AC:16:GLU:OE2	2.18	0.43
11:AL:315:LEU:HD13	11:AL:317:LEU:HD12	2.01	0.43
11:AM:462:ILE:HD12	11:AM:462:ILE:HA	1.83	0.43
11:AN:329:MET:O	11:AO:329:MET:HG2	2.17	0.43
11:AQ:293:THR:HG22	11:AQ:297:ARG:NH2	2.32	0.43
1:0:160:LEU:HD12	1:0:227:GLU:HA	2.00	0.43
2:1:108:PRO:HB3	11:AB:37:PRO:HD3	2.00	0.43
3:A:100:ARG:O	3:A:101:LEU:HB3	2.18	0.43
3:B:6:LYS:O	3:B:150:PHE:HB2	2.18	0.43
3:E:24:GLN:NE2	3:E:26:ARG:HD3	2.34	0.43
3:F:207:LYS:HA	9:J:69:ASN:OD1	2.18	0.43
5:H:114:ARG:HD2	5:R:32:VAL:HG22	2.00	0.43
6:I:93:LYS:HG3	6:I:94:HIS:HD1	1.83	0.43
1:N:159:GLU:OE2	1:N:228:ALA:HB1	2.18	0.43
7:U:72:PHE:HD1	7:U:72:PHE:HA	1.70	0.43
1:X:454:THR:OG1	1:X:462:GLN:HB3	2.18	0.43
2:Y:98:GLY:O	11:AQ:38:PRO:HA	2.19	0.43
8:Z:186:VAL:HB	8:j:193:LEU:HD12	2.00	0.43
1:f:410:ASN:OD1	2:p:116:THR:HG21	2.19	0.43
4:k:123:ARG:HD2	4:k:123:ARG:N	2.33	0.43
6:m:46:PHE:HD1	6:m:52:PRO:HA	1.84	0.43
11:AG:333:ASP:HB3	11:AG:336:ALA:H	1.83	0.43
11:AB:384:LYS:HB3	11:AC:390:ASP:OD1	2.18	0.43
11:AH:87:CYS:HB2	11:AH:107:TRP:CZ3	2.53	0.43
11:AK:21:VAL:HG23	11:AK:40:GLN:HB3	2.00	0.43
11:AK:179:THR:O	11:AL:171:SER:HA	2.19	0.43
11:AK:328:VAL:HB	11:AK:332:ALA:HB2	2.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:AL:277:LEU:HD23	11:AM:268:ASN:HD22	1.84	0.43
11:AQ:186:GLN:HG2	11:AQ:190:LEU:HG	1.99	0.43
2:1:66:ILE:O	2:1:70:ILE:HG13	2.17	0.43
3:D:92:ILE:HB	3:D:127:GLN:HE22	1.83	0.43
3:E:143:MET:HG3	3:E:148:GLU:HB3	2.00	0.43
8:P:144:HIS:CG	8:P:164:ARG:HH22	2.36	0.43
5:R:108:TRP:HZ2	5:b:40:LYS:HD3	1.83	0.43
6:S:17:TYR:CE1	6:S:32:PHE:HB2	2.54	0.43
2:Y:189:LEU:HD12	2:Y:189:LEU:HA	1.81	0.43
4:k:33:LEU:HD12	4:k:33:LEU:HA	1.87	0.43
6:y:31:GLN:HB3	6:y:44:ASP:OD1	2.18	0.43
11:AF:321:ALA:HB2	11:AG:321:ALA:HB1	2.01	0.43
11:AG:226:ALA:HA	11:AG:231:LYS:NZ	2.34	0.43
11:AB:222:PRO:HD3	11:AD:218:LYS:O	2.18	0.43
11:AI:282:LEU:HA	11:AJ:275:LYS:HZ1	1.83	0.43
11:AJ:401:MET:HE3	11:AJ:403:PHE:HE1	1.83	0.43
11:AO:312:ARG:HA	11:AO:315:LEU:HD12	2.01	0.43
11:AQ:462:ILE:HG23	11:AS:483:TRP:CE3	2.53	0.43
2:1:139:ARG:NH2	1:g:298:VAL:HG13	2.34	0.43
2:1:145:GLU:O	2:1:149:GLU:HG2	2.19	0.43
3:B:84:PHE:HA	3:B:87:THR:HG23	2.01	0.43
3:C:174:PHE:N	3:C:174:PHE:CD1	2.87	0.43
3:D:6:LYS:NZ	3:D:151:SER:HB2	2.34	0.43
3:D:195:PHE:HB3	9:d:2:LYS:HD2	2.00	0.43
1:N:398:LYS:HE2	1:N:462:GLN:HE21	1.83	0.43
1:V:208:GLN:HB3	1:V:213:PHE:HE1	1.83	0.43
1:W:403:ASN:CG	1:W:405:GLY:H	2.26	0.43
1:f:389:ARG:HG2	1:f:390:PRO:HD2	2.00	0.43
1:g:403:ASN:HA	1:g:407:MET:CE	2.48	0.43
1:o:379:ARG:NH2	2:p:160:VAL:HG12	2.33	0.43
1:o:407:MET:HG3	1:o:448:PHE:HB3	2.01	0.43
4:q:30:MET:HB2	4:q:59:ILE:HG12	2.01	0.43
5:r:66:GLN:HE21	5:r:66:GLN:HB3	1.61	0.43
7:t:11:ASP:OD2	2:v:26:LYS:HB3	2.18	0.43
4:w:15:ILE:HD12	4:w:25:VAL:HG21	2.01	0.43
11:AF:455:MET:HG3	11:AF:491:ASN:HD22	1.84	0.43
11:AB:257:MET:HG3	11:AB:258:PRO:HD2	2.01	0.43
11:AC:246:ARG:HA	11:AC:249:LEU:HB2	1.99	0.43
11:AC:416:ARG:HG3	11:AC:422:LEU:HD12	2.01	0.43
11:AD:203:ALA:HB3	11:AD:218:LYS:HG2	2.00	0.43
11:AD:406:ASN:HB3	11:AD:414:TRP:CE2	2.54	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:AH:222:PRO:HG2	11:AJ:215:ASN:HB3	1.99	0.43
11:AH:288:ALA:HB1	11:AJ:284:ILE:HG13	2.00	0.43
11:AI:488:TYR:HA	11:AI:489:PRO:HD3	1.93	0.43
11:AK:64:TRP:CH2	11:AK:95:ILE:HG12	2.53	0.43
11:AL:384:LYS:HG3	11:AM:390:ASP:HB2	1.99	0.43
11:AN:32:TRP:CZ3	11:AN:37:PRO:HB3	2.54	0.43
3:B:33:PRO:HA	3:B:39:LYS:HD2	2.00	0.43
3:C:12:LEU:HD23	3:C:12:LEU:HA	1.80	0.43
3:D:231:SER:HB2	6:s:87:LEU:HD13	2.00	0.43
3:F:176:GLU:HB2	4:w:43:ILE:HD11	2.00	0.43
1:M:397:ILE:HG12	1:M:455:ILE:HG22	2.00	0.43
1:W:12:LYS:HB2	1:W:62:TRP:CD1	2.54	0.43
2:Y:96:SER:O	2:Y:106:GLY:HA3	2.19	0.43
7:e:46:LEU:HD11	1:f:18:LEU:HD11	2.01	0.43
2:i:198:LYS:HA	2:i:204:TYR:CZ	2.53	0.43
1:o:399:ILE:HG13	1:o:484:VAL:HG13	1.99	0.43
5:r:157:LEU:HA	5:r:157:LEU:HD12	1.86	0.43
1:u:363:PHE:CE1	2:v:162:LEU:HD21	2.53	0.43
1:u:397:ILE:HA	1:u:455:ILE:HG22	2.00	0.43
9:d:294:TRP:N	9:d:294:TRP:CD1	2.86	0.43
11:AE:220:VAL:HG13	11:AF:222:PRO:HG3	2.00	0.43
11:AF:246:ARG:HA	11:AF:249:LEU:HD12	2.01	0.43
11:AC:177:GLN:HB2	11:AC:180:HIS:NE2	2.34	0.43
11:AH:329:MET:HE3	11:AH:330:MET:SD	2.59	0.43
11:AL:436:ARG:HD2	11:AM:458:PHE:HE2	1.83	0.43
11:AO:282:LEU:HA	11:AP:275:LYS:NZ	2.32	0.43
11:AO:343:THR:HB	11:AP:334:ASN:HD22	1.83	0.43
11:AP:272:VAL:HB	11:AP:275:LYS:HE2	2.00	0.43
11:AQ:89:ARG:HD2	11:AQ:106:TYR:HE1	1.83	0.43
11:AS:91:HIS:CE1	11:AS:94:LYS:HB2	2.54	0.43
1:0:188:LEU:HA	1:0:191:LEU:HD12	2.01	0.43
1:0:443:MET:HE3	1:N:437:ARG:HE	1.84	0.43
3:F:169:PHE:CE1	3:F:172:LEU:HD12	2.53	0.43
1:L:49:ARG:HA	7:U:44:TRP:CH2	2.54	0.43
1:L:115:SER:HB3	1:L:116:PRO:HD3	2.00	0.43
1:W:147:ILE:O	1:W:211:ILE:HG23	2.19	0.43
8:Z:241:THR:HG23	8:j:231:HIS:O	2.18	0.43
7:e:36:LYS:HD3	7:e:75:GLU:OE2	2.19	0.43
8:j:22:TYR:HB3	8:j:91:PHE:CD2	2.54	0.43
1:o:247:ILE:H	1:o:247:ILE:HD12	1.83	0.43
9:d:223:ILE:HD11	9:d:251:LEU:HD23	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:AB:436:ARG:HB2	11:AB:478:ARG:HD2	2.01	0.43
11:AC:116:GLU:O	11:AC:120:VAL:HG23	2.18	0.43
11:AC:175:ALA:HB2	11:AC:181:ALA:O	2.19	0.43
11:AC:394:LEU:HD13	11:AC:398:THR:HG21	2.01	0.43
11:AD:221:SER:OG	11:AD:224:LYS:HG2	2.19	0.43
11:AH:391:VAL:HG22	11:AI:401:MET:HG3	2.01	0.43
11:AI:278:ALA:O	11:AI:282:LEU:HB2	2.19	0.43
11:AJ:275:LYS:HB3	11:AJ:279:ARG:NH1	2.34	0.43
11:AK:228:VAL:O	11:AL:232:LYS:HB2	2.18	0.43
11:AK:463:GLY:H	11:AM:483:TRP:CB	2.32	0.43
11:AL:152:LYS:HE3	11:AL:152:LYS:HB2	1.76	0.43
11:AL:246:ARG:HA	11:AL:249:LEU:HD12	2.00	0.43
11:AM:455:MET:HG2	11:AM:490:PHE:HA	2.01	0.43
11:AQ:159:TYR:N	11:AR:162:LYS:HB2	2.34	0.43
11:AR:91:HIS:CE1	11:AR:94:LYS:HB2	2.54	0.43
11:AR:462:ILE:H	11:AR:485:ASN:HD21	1.66	0.43
11:AS:175:ALA:HB2	11:AS:181:ALA:O	2.19	0.43
1:0:297:PHE:HB3	1:0:299:GLN:OE1	2.19	0.43
1:L:167:ILE:HD13	1:L:167:ILE:HA	1.94	0.43
1:M:160:LEU:HB2	1:M:231:LEU:HD12	2.00	0.43
7:U:101:MET:HE3	7:U:101:MET:HB3	1.72	0.43
1:o:142:CYS:HB2	1:o:237:ARG:O	2.19	0.43
2:v:198:LYS:HG3	2:v:204:TYR:CE1	2.54	0.43
9:d:208:LYS:HE2	9:d:208:LYS:HB3	1.71	0.43
11:AG:177:GLN:HB2	11:AG:180:HIS:CE1	2.54	0.43
11:AC:320:MET:HA	11:AC:323:THR:OG1	2.19	0.43
11:AH:29:GLY:HA2	11:AI:16:GLU:OE1	2.19	0.43
11:AH:235:ASN:HA	11:AJ:239:LEU:HD22	2.01	0.43
11:AK:416:ARG:HG3	11:AK:417:LEU:N	2.33	0.43
11:AL:457:THR:HG22	11:AL:458:PHE:H	1.84	0.43
11:AM:165:ASN:HB3	11:AM:168:ASN:OD1	2.18	0.43
11:AN:254:THR:O	11:AP:254:THR:HB	2.18	0.43
11:AR:158:ARG:NH2	11:AS:155:GLY:HA2	2.33	0.43
11:AS:431:LEU:HD11	11:AS:437:THR:HG22	2.01	0.43
1:0:49:ARG:HH21	2:1:20:THR:HG21	1.82	0.42
1:0:207:GLU:HB2	1:0:212:LEU:HD12	2.01	0.42
2:1:81:ASP:HB3	2:1:84:ASN:HB3	2.00	0.42
6:I:81:LEU:O	6:I:106:LEU:HD12	2.18	0.42
1:L:81:ALA:O	1:L:85:LEU:HB2	2.19	0.42
1:M:302:ASN:OD1	1:o:303:ILE:HD11	2.17	0.42
8:Z:142:TRP:HZ3	8:Z:160:GLU:HB2	1.84	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:a:81:ARG:NH2	4:k:55:LEU:HD11	2.34	0.42
1:h:156:LEU:N	1:h:176:SER:HB3	2.32	0.42
1:h:299:GLN:H	2:v:139:ARG:HH22	1.65	0.42
1:h:454:THR:OG1	1:h:462:GLN:HB3	2.19	0.42
2:i:86:PHE:HD2	2:i:87:GLY:H	1.66	0.42
2:i:88:PHE:N	2:i:109:TRP:HB3	2.34	0.42
1:o:17:ILE:HD13	1:o:58:ASP:HB3	2.01	0.42
1:o:183:THR:HG22	1:o:185:GLU:H	1.84	0.42
1:u:454:THR:HB	1:u:462:GLN:HB3	2.01	0.42
2:v:176:LYS:NZ	2:v:177:ILE:H	2.14	0.42
11:AC:417:LEU:HD23	11:AC:417:LEU:HA	1.86	0.42
11:AD:433:ASP:HB2	11:AD:484:GLY:O	2.18	0.42
11:AH:236:LEU:HD13	11:AI:236:LEU:HD11	2.01	0.42
11:AI:424:GLN:OE1	11:AI:441:LEU:HB3	2.19	0.42
11:AL:431:LEU:HD11	11:AL:437:THR:HG22	2.01	0.42
11:AO:297:ARG:HB3	11:AO:297:ARG:HH11	1.83	0.42
11:AQ:455:MET:SD	11:AQ:491:ASN:HB3	2.59	0.42
11:AR:195:THR:HG23	11:AR:198:VAL:O	2.19	0.42
11:AR:349:GLY:HA3	11:AS:345:ARG:HH21	1.83	0.42
3:C:80:ASN:OD1	3:C:82:LYS:HB3	2.19	0.42
3:F:62:PHE:CE2	4:k:87:ARG:HG3	2.53	0.42
3:F:188:MET:HE2	3:F:188:MET:HB3	1.96	0.42
1:M:374:GLN:HE22	1:M:384:ARG:HG3	1.84	0.42
1:V:407:MET:HG2	1:V:408:PRO:O	2.19	0.42
8:Z:149:LEU:HA	8:j:78:SER:O	2.18	0.42
1:f:292:PHE:O	1:f:293:ARG:HB3	2.19	0.42
1:g:129:PHE:CE1	1:g:244:ASP:HB2	2.53	0.42
5:l:77:LEU:HD23	5:l:89:PHE:CE2	2.55	0.42
2:p:87:GLY:CA	2:p:109:TRP:HA	2.47	0.42
2:v:174:ILE:HG21	2:v:178:LEU:HD21	2.00	0.42
9:T:203:ASN:HA	9:T:274:ARG:NH1	2.34	0.42
11:AE:120:VAL:HG11	11:AG:120:VAL:HG11	1.99	0.42
11:AE:179:THR:O	11:AF:171:SER:HA	2.19	0.42
11:AF:194:ALA:HB2	11:AF:202:MET:HG2	2.01	0.42
11:AF:255:ALA:HB2	11:AG:255:ALA:HA	2.01	0.42
11:AC:312:ARG:HG2	11:AC:317:LEU:HB2	2.00	0.42
11:AH:225:ALA:HB1	11:AJ:229:TYR:HE2	1.85	0.42
11:AH:329:MET:CB	11:AI:330:MET:H	2.24	0.42
11:AK:241:ASN:HB3	11:AK:244:ALA:HB3	2.00	0.42
11:AM:394:LEU:HD22	11:AM:394:LEU:HA	1.92	0.42
11:AP:131:TYR:O	11:AP:134:LEU:HD22	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:0:468:GLU:H	1:0:468:GLU:HG3	1.60	0.42
2:1:136:ILE:HD13	2:1:136:ILE:HA	1.90	0.42
3:B:156:ARG:HE	4:G:44:ARG:NH2	2.17	0.42
3:E:100:ARG:O	3:E:101:LEU:HB3	2.18	0.42
3:F:207:LYS:HA	9:J:69:ASN:ND2	2.34	0.42
6:I:34:TRP:CZ2	6:I:39:ARG:HA	2.54	0.42
1:L:303:ILE:H	1:L:303:ILE:HG13	1.48	0.42
1:M:440:ALA:O	1:M:444:GLU:HG3	2.19	0.42
8:P:93:GLN:NE2	8:j:22:TYR:HA	2.31	0.42
1:V:293:ARG:HE	1:V:296:LYS:NZ	2.15	0.42
1:V:363:PHE:CZ	2:Y:170:VAL:HG21	2.54	0.42
1:W:129:PHE:CE1	1:W:244:ASP:HB2	2.54	0.42
1:o:202:THR:HG23	1:o:203:LEU:HG	2.02	0.42
1:o:203:LEU:HA	1:o:216:PRO:HA	2.01	0.42
7:z:33:LEU:HD23	7:z:33:LEU:HA	1.79	0.42
9:J:146:LEU:HD23	9:J:146:LEU:HA	1.90	0.42
11:AE:345:ARG:HG3	11:AE:350:LEU:HD12	2.02	0.42
11:AE:413:GLY:HA3	11:AE:425:TRP:NE1	2.34	0.42
11:AD:421:LEU:HD23	11:AD:421:LEU:HA	1.87	0.42
11:AH:84:ILE:HG22	11:AH:110:ALA:HB3	2.00	0.42
11:AH:367:ASN:HD21	11:AJ:373:ASN:H	1.67	0.42
11:AH:417:LEU:HD23	11:AH:417:LEU:HA	1.88	0.42
11:AI:69:GLU:HG2	11:AI:91:HIS:O	2.19	0.42
11:AI:112:GLU:OE2	11:AI:116:GLU:HG3	2.20	0.42
11:AM:315:LEU:HD23	11:AM:315:LEU:HA	1.84	0.42
11:AO:158:ARG:HB3	11:AP:158:ARG:O	2.19	0.42
11:AP:275:LYS:HD3	11:AP:275:LYS:HA	1.71	0.42
11:AR:81:ASN:OD1	11:AR:83:ILE:HG13	2.19	0.42
11:AR:319:GLY:O	11:AR:323:THR:HG23	2.19	0.42
2:1:31:ARG:HD3	1:g:32:LEU:HD22	2.01	0.42
3:D:174:PHE:N	3:D:174:PHE:HD1	2.17	0.42
3:F:131:LYS:CD	7:z:66:PRO:HB3	2.49	0.42
4:Q:117:THR:HG23	4:Q:119:GLY:H	1.85	0.42
5:R:88:LYS:HB3	5:R:106:THR:HG23	2.01	0.42
1:V:162:MET:HE2	1:V:162:MET:HB3	1.88	0.42
1:V:325:ASN:HD21	1:V:338:GLY:HA2	1.84	0.42
2:Y:108:PRO:HB2	2:Y:110:TYR:CD2	2.54	0.42
8:j:115:LYS:HE2	10:AA:784:GLN:HE22	1.85	0.42
4:k:79:GLN:HG2	4:k:79:GLN:H	1.61	0.42
6:m:17:TYR:N	6:m:17:TYR:CD1	2.87	0.42
5:r:88:LYS:HB3	5:r:106:THR:HG23	2.00	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:t:69:ASP:O	7:t:73:GLN:HG2	2.19	0.42
9:T:176:LYS:HB3	9:T:176:LYS:HE2	1.82	0.42
11:AE:115:GLY:H	11:AG:112:GLU:CD	2.27	0.42
11:AE:171:SER:H	11:AF:164:GLY:HA3	1.85	0.42
11:AE:302:LEU:HD23	11:AE:302:LEU:HA	1.90	0.42
11:AE:459:ASN:H	11:AG:482:ASN:ND2	2.18	0.42
11:AB:55:HIS:CE1	11:AC:6:LYS:HB2	2.54	0.42
11:AB:98:ASP:OD2	11:AB:100:LEU:HB2	2.19	0.42
11:AH:337:GLY:HA2	11:AI:331:LYS:NZ	2.35	0.42
11:AI:150:TYR:H	11:AJ:151:SER:HA	1.83	0.42
11:AI:421:LEU:HD23	11:AI:421:LEU:HA	1.85	0.42
11:AO:159:TYR:HA	11:AP:161:MET:HA	2.01	0.42
11:AO:339:ALA:HB2	11:AP:331:LYS:HE2	2.01	0.42
11:AP:410:ILE:H	11:AP:410:ILE:HG13	1.45	0.42
11:AQ:64:TRP:CH2	11:AQ:95:ILE:HG12	2.54	0.42
11:AR:480:SER:OG	11:AS:457:THR:HA	2.19	0.42
2:1:87:GLY:HA3	2:1:109:TRP:HA	2.01	0.42
3:D:96:ILE:HD11	4:q:20:TYR:CG	2.55	0.42
5:H:136:ASN:ND2	5:H:165:GLY:HA3	2.34	0.42
7:K:64:SER:HB2	7:K:66:PRO:HG2	2.01	0.42
1:M:414:ILE:O	1:M:417:PRO:HD2	2.19	0.42
2:O:112:VAL:HG22	11:AF:38:PRO:HB2	2.01	0.42
4:Q:26:VAL:HG12	4:Q:62:GLU:O	2.19	0.42
1:V:18:LEU:HB3	1:V:22:ARG:NH1	2.34	0.42
1:V:471:PHE:CZ	1:V:472:LYS:HE3	2.55	0.42
1:X:26:SER:HA	1:X:39:VAL:HG21	2.02	0.42
8:Z:145:ASP:HB2	8:Z:148:ASP:OD2	2.20	0.42
1:f:161:LYS:HB2	1:f:226:GLU:HB2	2.01	0.42
1:f:205:SER:HB2	1:f:212:LEU:HD21	2.01	0.42
2:i:88:PHE:HD1	2:i:107:ALA:O	2.03	0.42
5:l:1:MET:HE2	5:l:1:MET:HB2	1.90	0.42
7:n:33:LEU:HD23	7:n:33:LEU:HA	1.85	0.42
1:o:298:VAL:HG23	1:o:299:GLN:H	1.84	0.42
2:p:109:TRP:CD1	2:p:109:TRP:N	2.84	0.42
4:q:10:PRO:HD2	5:x:52:TYR:O	2.19	0.42
6:s:43:MET:HE3	6:s:43:MET:HB3	1.91	0.42
2:v:151:TYR:CE2	2:v:160:VAL:HB	2.55	0.42
4:w:26:VAL:HG12	4:w:62:GLU:O	2.19	0.42
9:T:207:THR:HG23	9:T:261:LEU:HG	2.01	0.42
11:AF:446:ARG:HG2	11:AF:497:SER:O	2.19	0.42
11:AJ:55:HIS:CE1	11:AJ:63:GLU:HB2	2.55	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:AJ:406:ASN:HB3	11:AJ:414:TRP:CE2	2.55	0.42
11:AJ:406:ASN:HB3	11:AJ:414:TRP:NE1	2.34	0.42
11:AK:452:VAL:HG12	11:AK:492:TRP:HB3	2.01	0.42
11:AM:231:LYS:HB2	11:AM:234:ASP:HB2	2.02	0.42
11:AN:55:HIS:CE1	11:AO:6:LYS:HB2	2.54	0.42
11:AQ:27:LYS:HA	11:AQ:27:LYS:HD2	1.86	0.42
11:AQ:296:LEU:HD23	11:AQ:296:LEU:HA	1.94	0.42
3:B:186:PRO:HB2	3:B:188:MET:HE3	2.02	0.42
1:L:221:ASN:HD21	1:L:372:GLU:HB3	1.84	0.42
2:O:84:ASN:ND2	2:O:120:ARG:HD3	2.35	0.42
8:P:244:PRO:HD3	8:Z:229:HIS:O	2.19	0.42
1:V:326:ASP:HB2	1:W:366:GLY:N	2.34	0.42
1:V:410:ASN:HD21	2:i:116:THR:HA	1.83	0.42
1:X:298:VAL:H	2:i:139:ARG:HH21	1.64	0.42
2:Y:88:PHE:CB	2:Y:109:TRP:HB3	2.50	0.42
5:b:12:VAL:HG22	5:b:93:ILE:HG12	2.00	0.42
1:f:379:ARG:HH12	2:i:148:ILE:HD12	1.85	0.42
4:k:74:PHE:CZ	4:q:136:THR:HA	2.55	0.42
6:m:83:MET:HE3	6:m:84:PRO:HD2	2.02	0.42
1:o:412:GLU:CD	1:o:412:GLU:H	2.27	0.42
1:o:429:ILE:HA	1:o:474:VAL:HG23	2.01	0.42
1:o:471:PHE:CZ	1:o:472:LYS:HE3	2.54	0.42
4:w:9:SER:HB2	4:w:12:ASP:OD2	2.20	0.42
5:x:1:MET:HE2	5:x:1:MET:HB2	1.87	0.42
9:T:47:SER:O	9:T:191:ASN:HB3	2.18	0.42
11:AE:257:MET:SD	11:AE:258:PRO:HD2	2.60	0.42
11:AG:85:TYR:CD2	11:AG:96:PRO:HB2	2.55	0.42
11:AB:88:LEU:HB2	11:AB:105:GLY:O	2.20	0.42
11:AL:91:HIS:CD2	11:AL:106:TYR:HD2	2.38	0.42
11:AM:75:SER:HB2	11:AM:87:CYS:HB3	2.00	0.42
11:AN:302:LEU:HD11	11:AP:302:LEU:HD11	2.02	0.42
11:AP:85:TYR:CD2	11:AP:96:PRO:HB2	2.55	0.42
11:AP:226:ALA:HA	11:AP:231:LYS:NZ	2.34	0.42
11:AQ:330:MET:HB3	11:AS:330:MET:O	2.20	0.42
11:AQ:392:TRP:O	11:AR:403:PHE:HB2	2.20	0.42
11:AR:74:LEU:HD22	11:AR:74:LEU:HA	1.88	0.42
11:AR:159:TYR:CD1	11:AS:160:ALA:HB3	2.54	0.42
11:AR:349:GLY:HA3	11:AS:345:ARG:NH2	2.34	0.42
3:A:96:ILE:HG22	3:A:122:ALA:HA	2.01	0.42
3:F:72:ASN:O	3:F:76:THR:HG23	2.20	0.42
1:V:342:LEU:HD11	1:V:388:GLN:HE21	1.85	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:f:18:LEU:HB3	1:f:22:ARG:NH1	2.34	0.42
1:f:127:ARG:HD3	1:f:127:ARG:HA	1.84	0.42
1:f:363:PHE:CE1	2:i:162:LEU:HD21	2.54	0.42
1:h:4:ILE:HD11	2:v:63:GLN:NE2	2.34	0.42
8:j:93:GLN:HG3	8:j:94:ARG:HE	1.84	0.42
1:o:399:ILE:HD11	1:o:484:VAL:HG22	2.02	0.42
2:p:33:LEU:HA	2:p:33:LEU:HD23	1.80	0.42
1:u:439:TYR:O	1:u:443:MET:HG2	2.19	0.42
2:v:126:GLU:O	2:v:130:ILE:HG22	2.20	0.42
6:y:17:TYR:CD1	6:y:17:TYR:N	2.87	0.42
9:d:4:TYR:CD2	9:d:5:ASP:HB2	2.55	0.42
9:d:71:LEU:HD23	9:d:71:LEU:HA	1.78	0.42
11:AE:203:ALA:HB3	11:AE:218:LYS:HD2	2.01	0.42
11:AE:327:ALA:HA	11:AF:331:LYS:HB2	2.01	0.42
11:AG:307:ASN:ND2	11:AG:310:GLN:HG2	2.34	0.42
11:AH:115:GLY:H	11:AJ:112:GLU:CD	2.28	0.42
11:AI:194:ALA:HB2	11:AI:202:MET:HG2	2.02	0.42
11:AI:288:ALA:HB2	11:AJ:288:ALA:HB1	2.00	0.42
11:AJ:85:TYR:CD2	11:AJ:96:PRO:HB2	2.55	0.42
11:AK:160:ALA:HB3	11:AL:159:TYR:OH	2.19	0.42
11:AM:406:ASN:HB3	11:AM:414:TRP:CE2	2.55	0.42
11:AN:459:ASN:H	11:AP:482:ASN:ND2	2.17	0.42
11:AQ:329:MET:C	11:AQ:331:LYS:H	2.27	0.42
11:AQ:410:ILE:H	11:AQ:410:ILE:HG13	1.52	0.42
11:AR:152:LYS:HE2	11:AR:152:LYS:HB2	1.87	0.42
1:0:262:ILE:HA	1:0:263:PRO:HD3	1.90	0.42
1:L:155:ASP:HB2	1:L:178:ALA:HA	2.01	0.42
1:L:208:GLN:HB3	1:L:213:PHE:HE1	1.85	0.42
1:M:91:ILE:HD13	1:M:91:ILE:HA	1.87	0.42
1:N:172:ILE:HG12	1:N:195:VAL:HG22	2.02	0.42
2:O:39:GLY:O	2:O:43:ILE:HG12	2.20	0.42
2:O:189:LEU:HD12	2:O:189:LEU:HA	1.83	0.42
1:V:145:VAL:HG21	1:V:225:PHE:CG	2.54	0.42
1:W:296:LYS:HE2	1:W:296:LYS:HB2	1.79	0.42
2:Y:184:SER:O	2:Y:189:LEU:HB2	2.19	0.42
1:g:147:ILE:O	1:g:211:ILE:HG23	2.19	0.42
1:g:307:LEU:HD13	1:g:360:ASN:HB3	2.00	0.42
2:i:109:TRP:O	2:i:109:TRP:CD1	2.73	0.42
2:p:184:SER:O	2:p:189:LEU:HB2	2.20	0.42
9:J:264:VAL:O	9:J:270:SER:HA	2.20	0.42
9:T:237:LYS:HB2	9:T:237:LYS:HE3	1.76	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:AB:216:ASP:HA	11:AC:221:SER:HB3	2.02	0.42
11:AB:298:SER:H	11:AD:295:PHE:HA	1.85	0.42
11:AH:179:THR:O	11:AI:171:SER:HA	2.19	0.42
11:AI:137:ILE:H	11:AI:137:ILE:HD12	1.84	0.42
11:AL:159:TYR:HD1	11:AL:160:ALA:H	1.67	0.42
11:AL:229:TYR:HE1	11:AM:225:ALA:HB1	1.85	0.42
11:AM:422:LEU:HB3	11:AM:424:GLN:OE1	2.19	0.42
11:AO:19:GLN:OE1	11:AO:21:VAL:HG23	2.20	0.42
11:AO:175:ALA:HB2	11:AO:181:ALA:O	2.19	0.42
11:AO:450:VAL:HG11	11:AO:469:THR:HG21	2.02	0.42
1:O:410:ASN:OD1	2:O:116:THR:HG22	2.20	0.42
3:A:230:THR:HA	1:V:290:GLU:OE2	2.20	0.42
3:B:82:LYS:HG3	7:K:86:THR:HG22	2.02	0.42
3:B:217:ARG:CD	3:B:218:ASP:H	2.33	0.42
1:L:363:PHE:HZ	2:O:162:LEU:HD11	1.83	0.42
1:L:446:PRO:HA	1:W:437:ARG:NH1	2.34	0.42
1:N:148:PHE:CE1	1:W:253:GLN:HA	2.54	0.42
2:O:73:ARG:HB2	2:O:134:LYS:HG2	2.02	0.42
8:P:59:GLN:HE22	9:T:172:ARG:NH1	2.18	0.42
4:Q:15:ILE:HG12	4:Q:92:VAL:HG12	2.01	0.42
4:Q:90:LEU:HD12	4:Q:90:LEU:HA	1.85	0.42
1:V:408:PRO:HA	2:i:116:THR:OG1	2.19	0.42
1:V:412:GLU:CD	1:V:412:GLU:H	2.27	0.42
1:W:298:VAL:HG13	2:Y:139:ARG:NH2	2.34	0.42
1:W:397:ILE:HG12	1:W:455:ILE:HG22	2.01	0.42
1:X:359:LEU:HA	1:X:359:LEU:HD12	1.85	0.42
1:h:198:ASN:HB3	1:h:199:HIS:ND1	2.34	0.42
1:h:400:SER:HB3	1:h:452:SER:HB3	2.02	0.42
7:n:111:THR:HG23	7:n:112:GLU:HG3	2.02	0.42
1:u:292:PHE:C	1:u:294:ASN:H	2.28	0.42
7:z:61:LYS:HD3	7:z:61:LYS:HA	1.56	0.42
9:T:37:LEU:HD23	9:T:37:LEU:HA	1.95	0.42
9:d:273:PHE:HD1	9:d:297:ASP:HA	1.85	0.42
11:AE:451:GLN:NE2	11:AF:493:PHE:HB3	2.34	0.42
11:AF:58:GLN:HG2	11:AF:59:HIS:HD2	1.85	0.42
11:AB:210:THR:HG22	11:AB:228:VAL:HG21	2.02	0.42
11:AC:317:LEU:HD13	11:AD:317:LEU:HD22	2.02	0.42
11:AI:81:ASN:HD21	11:AI:83:ILE:HB	1.84	0.42
11:AI:446:ARG:HG2	11:AI:497:SER:O	2.20	0.42
11:AJ:94:LYS:HE2	11:AJ:106:TYR:CZ	2.55	0.42
11:AL:409:ASP:OD2	11:AL:411:SER:HB3	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:AM:449:ASN:ND2	11:AM:451:GLN:HE21	2.18	0.42
11:AO:150:TYR:CE1	11:AP:152:LYS:HA	2.55	0.42
11:AQ:288:ALA:HB1	11:AS:284:ILE:HG23	2.02	0.42
2:1:18:ARG:HD2	7:z:45:PHE:CD1	2.55	0.42
3:C:100:ARG:O	3:C:101:LEU:HB3	2.20	0.42
3:E:207:LYS:HA	9:T:69:ASN:OD1	2.20	0.42
1:L:303:ILE:HD12	1:L:304:LEU:H	1.85	0.42
1:M:158:TYR:HB3	1:M:231:LEU:HD21	2.02	0.42
1:M:363:PHE:CE1	1:o:324:GLU:HG2	2.55	0.42
1:M:429:ILE:HA	1:M:474:VAL:HB	2.00	0.42
2:O:151:TYR:CE2	2:O:160:VAL:HB	2.55	0.42
2:O:224:GLN:HG3	2:O:236:GLY:HA2	2.01	0.42
4:a:10:PRO:HD2	5:l:52:TYR:O	2.20	0.42
4:a:30:MET:HB2	4:a:59:ILE:HG12	2.02	0.42
6:c:73:HIS:CE1	6:c:74:ILE:HG12	2.55	0.42
1:o:11:ILE:HG22	1:o:62:TRP:HE3	1.85	0.42
1:o:408:PRO:HA	2:v:116:THR:OG1	2.20	0.42
9:J:245:GLY:HA2	9:J:296:SER:HA	2.02	0.42
11:AF:55:HIS:CE1	11:AG:6:LYS:HB2	2.55	0.42
11:AB:263:LEU:HD12	11:AC:263:LEU:HB3	2.02	0.42
11:AC:391:VAL:HG21	11:AC:394:LEU:HD12	2.02	0.42
11:AD:175:ALA:HB2	11:AD:181:ALA:O	2.20	0.42
11:AH:222:PRO:HB3	11:AJ:210:THR:HG23	2.02	0.42
11:AH:296:LEU:HD12	11:AI:296:LEU:HB3	2.00	0.42
11:AL:144:ARG:HA	11:AL:147:LEU:HD12	2.02	0.42
11:AL:169:VAL:O	11:AM:163:HIS:HA	2.19	0.42
11:AR:317:LEU:HD22	11:AS:317:LEU:HD21	2.02	0.42
11:AS:424:GLN:OE1	11:AS:441:LEU:HB3	2.20	0.42
1:O:142:CYS:HB2	1:O:237:ARG:O	2.20	0.41
3:C:29:VAL:HG13	3:C:44:ILE:HG23	2.01	0.41
1:M:394:PRO:HG2	1:M:458:LYS:HB3	2.01	0.41
1:N:299:GLN:O	1:N:301:THR:HG23	2.20	0.41
1:N:396:GLU:HA	1:N:481:ASP:HB3	2.02	0.41
2:Y:80:GLN:HG3	2:Y:82:ILE:H	1.85	0.41
6:c:103:PHE:HE1	1:u:31:ASP:HA	1.85	0.41
1:g:140:LYS:HE3	1:g:140:LYS:HB3	1.86	0.41
1:h:321:ARG:NH1	1:h:430:GLY:HA3	2.35	0.41
5:l:33:LYS:HG3	5:l:58:TRP:CZ2	2.55	0.41
9:d:27:HIS:CE1	9:d:33:ASN:HD22	2.37	0.41
9:d:95:GLY:HA3	9:d:116:GLY:O	2.20	0.41
11:AE:417:LEU:HD23	11:AE:417:LEU:HA	1.89	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:AE:422:LEU:HD22	11:AE:424:GLN:HE21	1.85	0.41
11:AB:307:ASN:HD21	11:AB:309:ALA:HB3	1.85	0.41
11:AD:417:LEU:HD12	11:AD:421:LEU:HD12	2.02	0.41
11:AH:463:GLY:H	11:AJ:483:TRP:CB	2.31	0.41
11:AJ:221:SER:OG	11:AJ:224:LYS:HG2	2.20	0.41
11:AJ:431:LEU:HA	11:AJ:431:LEU:HD23	1.82	0.41
11:AK:55:HIS:CE1	11:AL:6:LYS:HB2	2.55	0.41
11:AL:175:ALA:HB2	11:AL:181:ALA:O	2.20	0.41
11:AM:175:ALA:HB2	11:AM:181:ALA:O	2.19	0.41
11:AM:366:ASP:HB3	11:AM:369:SER:HB3	2.02	0.41
11:AN:159:TYR:N	11:AO:162:LYS:HB2	2.35	0.41
11:AN:255:ALA:HB1	11:AP:255:ALA:HB2	2.02	0.41
11:AQ:13:ILE:HB	11:AQ:16:GLU:HB2	2.01	0.41
11:AR:231:LYS:HB2	11:AR:234:ASP:CG	2.45	0.41
11:AR:311:ALA:HA	11:AS:301:ASN:HB3	2.02	0.41
2:1:109:TRP:CE3	11:AC:36:LEU:HD12	2.53	0.41
3:A:174:PHE:N	3:A:174:PHE:CD1	2.87	0.41
3:B:204:ARG:HD3	6:y:16:LYS:O	2.20	0.41
3:D:140:LEU:HD23	3:D:140:LEU:HA	1.79	0.41
4:G:55:LEU:HA	4:G:55:LEU:HD23	1.87	0.41
1:L:18:LEU:HB3	1:L:22:ARG:NH1	2.35	0.41
1:L:408:PRO:HB3	2:Y:116:THR:H	1.84	0.41
1:N:147:ILE:HD13	1:N:147:ILE:HA	1.90	0.41
2:O:62:LYS:HE3	2:O:62:LYS:HB3	1.84	0.41
8:P:148:ASP:HB3	8:P:166:LYS:HA	2.02	0.41
4:Q:156:SER:O	4:Q:159:ARG:HG3	2.20	0.41
1:V:211:ILE:HG23	1:V:234:GLN:NE2	2.35	0.41
1:V:412:GLU:O	1:V:416:ARG:HG3	2.20	0.41
1:W:120:MET:HB2	1:W:120:MET:HE3	1.80	0.41
1:W:453:LEU:HD23	1:W:454:THR:N	2.35	0.41
1:X:258:ASP:CG	1:X:259:THR:HG23	2.45	0.41
1:X:297:PHE:CE2	2:i:138:ASN:HA	2.55	0.41
1:X:321:ARG:NH1	1:X:430:GLY:HA3	2.36	0.41
1:X:322:ILE:HD13	1:X:322:ILE:HA	1.91	0.41
4:a:120:ILE:HG12	5:r:41:HIS:CG	2.55	0.41
1:o:56:PRO:HG2	2:p:18:ARG:HH12	1.85	0.41
1:o:116:PRO:HB2	1:o:117:PRO:HD3	2.03	0.41
1:o:173:LYS:HE2	1:o:173:LYS:HB3	1.86	0.41
1:o:363:PHE:CE1	2:p:162:LEU:HD21	2.55	0.41
10:5:697:ILE:HD13	10:5:697:ILE:HA	1.91	0.41
11:AB:482:ASN:CB	11:AC:459:ASN:H	2.34	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:AC:307:ASN:HD21	11:AC:309:ALA:HB3	1.85	0.41
11:AD:192:PRO:O	11:AD:200:GLY:HA3	2.20	0.41
11:AH:410:ILE:H	11:AH:410:ILE:HG13	1.51	0.41
11:AK:320:MET:HG2	11:AL:325:PRO:HB3	2.02	0.41
3:C:32:ASN:ND2	9:T:38:GLN:HG2	2.35	0.41
3:E:131:LYS:NZ	7:n:66:PRO:HA	2.35	0.41
1:X:67:MET:HE3	1:X:67:MET:HB2	1.98	0.41
2:Y:88:PHE:HA	2:Y:107:ALA:O	2.20	0.41
1:f:297:PHE:HB3	1:f:299:GLN:HB2	2.02	0.41
2:v:109:TRP:CD1	2:v:109:TRP:N	2.88	0.41
4:w:15:ILE:HG12	4:w:92:VAL:HG12	2.01	0.41
4:w:99:THR:HA	4:w:136:THR:O	2.19	0.41
9:d:237:LYS:HB2	9:d:237:LYS:HE3	1.79	0.41
11:AF:378:ARG:HG2	11:AF:383:LEU:HD12	2.03	0.41
11:AC:207:THR:OG1	11:AC:224:LYS:HE2	2.21	0.41
11:AC:449:ASN:ND2	11:AD:493:PHE:HB2	2.35	0.41
11:AI:35:GLU:O	11:AI:37:PRO:HD3	2.19	0.41
11:AK:6:LYS:HB2	11:AM:55:HIS:CD2	2.55	0.41
11:AM:233:LYS:H	11:AM:233:LYS:HG2	1.38	0.41
11:AN:152:LYS:HG2	11:AP:148:SER:OG	2.20	0.41
11:AN:317:LEU:HD13	11:AP:317:LEU:HD21	2.03	0.41
11:AQ:279:ARG:NH1	11:AS:283:GLY:HA3	2.36	0.41
11:AQ:493:PHE:HB3	11:AS:451:GLN:NE2	2.34	0.41
1:0:122:SER:HB2	1:0:257:ILE:HG22	2.03	0.41
1:0:408:PRO:HA	2:O:116:THR:OG1	2.20	0.41
3:C:62:PHE:CE2	4:a:87:ARG:HG3	2.55	0.41
3:F:84:PHE:HA	3:F:87:THR:HG23	2.01	0.41
5:H:51:VAL:HG12	4:w:8:TYR:HD2	1.85	0.41
1:L:428:LYS:HE2	1:L:428:LYS:HB3	1.91	0.41
1:L:443:MET:HB2	1:W:440:ALA:HB2	2.02	0.41
1:M:165:ASP:HB2	1:M:168:ASN:OD1	2.20	0.41
1:M:437:ARG:HH21	1:f:443:MET:HB3	1.85	0.41
8:P:22:TYR:HA	8:Z:93:GLN:OE1	2.20	0.41
6:S:2:SER:HB2	6:S:112:ASP:O	2.20	0.41
6:S:93:LYS:HG3	6:S:94:HIS:ND1	2.34	0.41
2:Y:39:GLY:O	2:Y:43:ILE:HG12	2.20	0.41
1:g:21:TYR:HD1	1:g:21:TYR:HA	1.78	0.41
2:i:26:LYS:HD3	2:i:26:LYS:HA	1.85	0.41
4:k:22:LEU:HA	4:k:22:LEU:HD12	1.87	0.41
1:o:310:GLY:O	1:o:314:VAL:HG23	2.20	0.41
2:p:80:GLN:HG3	2:p:82:ILE:H	1.86	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:s:65:ILE:HG23	6:s:80:PHE:HB2	2.02	0.41
11:AG:275:LYS:HA	11:AG:275:LYS:HD3	1.76	0.41
11:AB:179:THR:O	11:AC:171:SER:HA	2.21	0.41
11:AH:462:ILE:HG23	11:AJ:483:TRP:CD1	2.55	0.41
11:AI:120:VAL:HG11	11:AJ:120:VAL:HG11	2.03	0.41
11:AL:297:ARG:NH2	11:AL:300:GLN:HG2	2.35	0.41
11:AM:440:GLN:CD	11:AM:475:THR:HB	2.44	0.41
11:AR:10:ILE:HD12	11:AR:10:ILE:HA	1.91	0.41
3:A:174:PHE:N	3:A:174:PHE:HD1	2.18	0.41
3:B:234:SER:OG	3:B:235:PRO:HD3	2.20	0.41
3:E:222:GLY:O	3:E:228:ASN:HB3	2.21	0.41
3:E:230:THR:HG22	1:f:290:GLU:HG2	2.01	0.41
4:G:33:LEU:HA	4:G:33:LEU:HD12	1.79	0.41
1:N:213:PHE:HD1	1:N:213:PHE:HA	1.69	0.41
1:N:390:PRO:HB2	1:N:474:VAL:HG12	2.03	0.41
8:P:193:LEU:HD12	8:j:186:VAL:HB	2.01	0.41
6:S:17:TYR:N	6:S:17:TYR:HD1	2.17	0.41
7:U:63:ARG:HA	7:U:63:ARG:NH1	2.34	0.41
5:b:56:GLN:O	5:b:58:TRP:HD1	2.02	0.41
5:b:116:SER:H	5:b:124:ARG:NH1	2.18	0.41
1:f:337:PRO:HD2	1:f:368:VAL:HG11	2.02	0.41
1:g:61:ILE:O	1:g:65:ILE:HG12	2.20	0.41
1:g:140:LYS:HD2	1:g:141:ALA:N	2.35	0.41
1:g:437:ARG:HH21	1:u:443:MET:HB3	1.84	0.41
8:j:12:LEU:HD12	8:j:12:LEU:HA	1.81	0.41
7:t:38:TYR:HD1	7:t:38:TYR:HA	1.73	0.41
4:w:22:LEU:HD12	4:w:22:LEU:HA	1.93	0.41
9:T:252:LEU:HA	9:T:291:THR:OG1	2.20	0.41
11:AG:61:ILE:HB	11:AG:78:GLN:HB2	2.02	0.41
11:AB:64:TRP:CH2	11:AB:95:ILE:HG12	2.55	0.41
11:AD:94:LYS:HA	11:AD:94:LYS:HD3	1.89	0.41
11:AD:162:LYS:HE3	11:AD:162:LYS:HB2	1.83	0.41
11:AH:425:TRP:HB2	11:AJ:449:ASN:ND2	2.36	0.41
11:AK:293:THR:HG22	11:AK:297:ARG:NH2	2.35	0.41
11:AM:69:GLU:HG2	11:AM:91:HIS:O	2.20	0.41
11:AN:331:LYS:NZ	11:AP:328:VAL:HA	2.36	0.41
11:AR:311:ALA:O	11:AR:315:LEU:HB2	2.21	0.41
1:O:310:GLY:O	1:O:314:VAL:HG23	2.21	0.41
2:1:237:ILE:HD13	2:1:237:ILE:HA	1.98	0.41
3:B:210:LYS:H	3:B:210:LYS:HG2	1.63	0.41
3:B:210:LYS:HB3	3:B:210:LYS:HE3	1.68	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:174:PHE:N	3:C:174:PHE:HD1	2.18	0.41
4:G:120:ILE:H	4:G:120:ILE:HG13	1.55	0.41
6:I:84:PRO:HB3	6:I:104:PHE:CE2	2.56	0.41
1:M:159:GLU:O	1:M:228:ALA:HB3	2.21	0.41
1:M:298:VAL:HG13	2:p:139:ARG:NH2	2.35	0.41
1:N:31:ASP:HB2	2:O:31:ARG:NH2	2.36	0.41
1:V:12:LYS:HE2	1:V:62:TRP:CZ2	2.55	0.41
1:V:410:ASN:OD1	2:i:116:THR:HG22	2.21	0.41
1:V:437:ARG:HD3	1:X:443:MET:HE1	2.03	0.41
2:i:93:ARG:HG3	2:i:94:ALA:H	1.86	0.41
2:v:189:LEU:HD12	2:v:189:LEU:HA	1.88	0.41
9:d:74:GLU:HB3	9:d:75:TYR:CE2	2.55	0.41
10:6:697:ILE:HD13	10:6:697:ILE:HA	1.95	0.41
11:AE:331:LYS:O	11:AE:331:LYS:HD3	2.20	0.41
11:AF:141:VAL:O	11:AF:145:GLN:HG3	2.21	0.41
11:AC:410:ILE:H	11:AC:410:ILE:HG13	1.56	0.41
11:AD:13:ILE:HB	11:AD:16:GLU:HG2	2.02	0.41
11:AD:242:VAL:O	11:AD:246:ARG:HG3	2.21	0.41
11:AI:424:GLN:OE1	11:AI:442:PRO:HD2	2.20	0.41
11:AK:426:GLY:HA3	11:AK:492:TRP:CZ2	2.56	0.41
11:AN:279:ARG:HB3	11:AN:284:ILE:HB	2.03	0.41
11:AR:232:LYS:HB3	11:AR:233:LYS:NZ	2.35	0.41
1:0:379:ARG:NH2	2:1:160:VAL:HG12	2.36	0.41
2:1:184:SER:O	2:1:189:LEU:HB2	2.20	0.41
4:G:136:THR:HA	4:w:74:PHE:CZ	2.56	0.41
2:O:88:PHE:HD1	2:O:107:ALA:O	2.03	0.41
4:Q:8:TYR:HD2	5:b:51:VAL:HG12	1.85	0.41
1:X:445:ILE:HD12	1:X:446:PRO:HD2	2.01	0.41
2:Y:84:ASN:C	2:Y:117:GLY:HA2	2.46	0.41
8:Z:27:CYS:HA	8:Z:46:VAL:HG13	2.02	0.41
8:Z:136:ASP:CG	8:Z:138:ALA:H	2.28	0.41
1:h:234:GLN:HG3	1:h:235:LYS:HG3	2.03	0.41
1:h:258:ASP:CG	1:h:259:THR:HG23	2.45	0.41
2:i:78:VAL:HG12	2:i:120:ARG:O	2.21	0.41
2:i:126:GLU:O	2:i:130:ILE:HG22	2.21	0.41
1:u:154:ASN:HB3	1:u:178:ALA:O	2.21	0.41
1:u:158:TYR:HB3	1:u:231:LEU:HD21	2.03	0.41
5:x:15:ALA:HA	5:x:90:PRO:HG2	2.02	0.41
9:d:245:GLY:HA2	9:d:296:SER:HA	2.03	0.41
11:AE:329:MET:O	11:AF:329:MET:HG2	2.21	0.41
11:AI:246:ARG:HA	11:AI:249:LEU:HD12	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:AJ:139:ASN:OD1	11:AJ:142:ILE:HG12	2.21	0.41
11:AJ:177:GLN:HB2	11:AJ:180:HIS:CE1	2.55	0.41
11:AN:177:GLN:HB2	11:AN:180:HIS:CG	2.55	0.41
11:AQ:137:ILE:H	11:AQ:137:ILE:HD12	1.86	0.41
11:AQ:479:VAL:HG11	11:AQ:490:PHE:CZ	2.56	0.41
11:AR:409:ASP:CG	11:AR:411:SER:H	2.29	0.41
11:AR:461:SER:HB3	11:AR:485:ASN:ND2	2.36	0.41
1:0:394:PRO:HG2	1:0:458:LYS:HD3	2.03	0.41
3:A:96:ILE:HD11	4:G:20:TYR:HB3	2.03	0.41
3:E:72:ASN:O	3:E:76:THR:HG23	2.21	0.41
1:L:292:PHE:C	1:L:294:ASN:H	2.28	0.41
1:N:258:ASP:CG	1:N:259:THR:HG23	2.46	0.41
8:P:32:VAL:HA	8:P:41:VAL:HG12	2.01	0.41
5:R:92:MET:HE2	5:R:103:LEU:HD12	2.03	0.41
1:V:174:TYR:CZ	1:V:190:GLY:HA3	2.56	0.41
1:V:206:TYR:O	1:V:212:LEU:HG	2.20	0.41
1:V:372:GLU:OE2	1:V:384:ARG:HD3	2.21	0.41
1:X:4:ILE:HD11	2:i:63:GLN:CD	2.46	0.41
1:X:17:ILE:HD11	1:X:62:TRP:HD1	1.86	0.41
5:b:82:ILE:HD12	5:b:82:ILE:HA	1.94	0.41
7:e:61:LYS:HA	7:e:61:LYS:HD3	1.83	0.41
1:g:253:GLN:HG3	1:h:148:PHE:CD1	2.56	0.41
2:i:97:PHE:HE2	11:AP:37:PRO:HG2	1.85	0.41
8:j:136:ASP:CG	8:j:138:ALA:H	2.28	0.41
4:k:62:GLU:HG2	4:k:124:VAL:HG22	2.03	0.41
4:k:108:VAL:HA	4:k:127:ILE:HD13	2.03	0.41
6:m:77:ASN:HB2	6:m:110:ASN:HD21	1.85	0.41
2:p:66:ILE:O	2:p:70:ILE:HG13	2.21	0.41
11:AG:296:LEU:HD23	11:AG:296:LEU:HA	1.85	0.41
11:AB:422:LEU:HD11	11:AB:498:THR:HB	2.03	0.41
11:AD:381:LEU:HD23	11:AD:381:LEU:HA	1.91	0.41
11:AH:318:THR:HB	11:AI:325:PRO:HD3	2.03	0.41
11:AH:459:ASN:H	11:AJ:482:ASN:ND2	2.18	0.41
11:AL:253:ASP:O	11:AL:257:MET:HG3	2.20	0.41
11:AN:51:LEU:HD23	11:AO:7:PRO:HB3	2.03	0.41
11:AO:48:LYS:HE2	11:AO:48:LYS:HB3	1.87	0.41
11:AO:69:GLU:HG2	11:AO:91:HIS:O	2.21	0.41
11:AQ:451:GLN:NE2	11:AR:493:PHE:HB3	2.36	0.41
11:AR:52:PHE:CZ	11:AS:57:ASN:HB2	2.56	0.41
1:0:160:LEU:O	1:0:171:SER:HA	2.21	0.41
1:0:397:ILE:HG13	1:0:482:ILE:HG12	2.01	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:1:100:LEU:HD23	2:1:100:LEU:HA	1.75	0.41
3:A:34:ILE:HG23	3:A:43:HIS:CD2	2.55	0.41
3:C:6:LYS:NZ	3:C:151:SER:HB2	2.36	0.41
3:C:49:PRO:HD3	3:E:145:ARG:HH22	1.86	0.41
3:D:35:GLU:HB3	3:D:36:THR:O	2.21	0.41
6:I:16:LYS:HG3	6:I:33:TYR:HB3	2.02	0.41
6:I:34:TRP:NE1	6:I:36:SER:HA	2.36	0.41
6:I:43:MET:HE3	6:I:43:MET:HB3	1.94	0.41
1:L:173:LYS:HE2	1:L:173:LYS:HB3	1.87	0.41
1:L:299:GLN:HB3	1:N:299:GLN:OE1	2.21	0.41
1:M:120:MET:HE3	1:M:120:MET:HB2	1.78	0.41
2:O:208:GLU:HG3	2:O:240:ASN:HB2	2.02	0.41
8:P:9:LEU:HD23	8:P:9:LEU:HA	1.87	0.41
8:P:244:PRO:HB3	8:j:231:HIS:CE1	2.56	0.41
4:Q:22:LEU:HD12	4:Q:22:LEU:HA	1.83	0.41
5:R:143:GLN:C	5:R:145:LEU:H	2.28	0.41
7:U:38:TYR:HD1	7:U:38:TYR:HA	1.74	0.41
7:U:61:LYS:HZ1	7:U:97:ARG:HG3	1.86	0.41
1:V:292:PHE:CG	1:V:293:ARG:N	2.89	0.41
1:X:144:GLY:HA3	1:X:215:VAL:HG12	2.03	0.41
6:c:11:LEU:HD23	6:c:11:LEU:HA	1.91	0.41
7:e:101:MET:HE3	7:e:101:MET:HB3	1.78	0.41
1:f:363:PHE:HZ	2:i:162:LEU:HD11	1.84	0.41
1:g:394:PRO:HG2	1:g:458:LYS:HB3	2.03	0.41
1:g:440:ALA:O	1:g:444:GLU:HG3	2.21	0.41
2:i:36:LEU:HD13	2:i:36:LEU:HA	1.91	0.41
2:i:87:GLY:HA2	11:AO:36:LEU:HD11	2.02	0.41
1:o:160:LEU:HD12	1:o:227:GLU:HA	2.02	0.41
2:p:100:LEU:HD23	2:p:100:LEU:HA	1.78	0.41
5:r:155:SER:HB3	5:r:156:LEU:HD12	2.02	0.41
6:s:50:LEU:HD13	6:s:50:LEU:HA	1.91	0.41
2:v:93:ARG:HG3	2:v:94:ALA:H	1.85	0.41
2:v:217:THR:HG22	2:v:218:GLU:H	1.85	0.41
7:z:59:LEU:HA	7:z:59:LEU:HD13	1.83	0.41
9:T:4:TYR:CD2	9:T:5:ASP:HB2	2.56	0.41
9:T:142:GLU:OE2	9:T:153:ARG:HD2	2.21	0.41
9:d:121:ALA:O	9:d:148:MET:HE3	2.21	0.41
11:AE:98:ASP:OD2	11:AE:100:LEU:HB2	2.21	0.41
11:AE:152:LYS:NZ	11:AG:148:SER:HA	2.36	0.41
11:AF:436:ARG:HG3	11:AF:478:ARG:HD2	2.03	0.41
11:AF:447:ILE:HG12	11:AF:496:THR:HG22	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:AG:221:SER:OG	11:AG:224:LYS:HG2	2.21	0.41
11:AB:320:MET:HB2	11:AC:323:THR:O	2.21	0.41
11:AC:175:ALA:HB1	11:AD:184:LEU:HB2	2.03	0.41
11:AC:186:GLN:HG2	11:AC:190:LEU:HG	2.03	0.41
11:AC:242:VAL:HG12	11:AC:246:ARG:HH11	1.86	0.41
11:AC:471:MET:HG3	11:AC:478:ARG:NH2	2.36	0.41
11:AD:233:LYS:H	11:AD:233:LYS:HG2	1.53	0.41
11:AH:36:LEU:O	11:AH:38:PRO:HD3	2.21	0.41
11:AH:49:GLN:HE22	11:AI:46:GLU:HG3	1.86	0.41
11:AJ:15:SER:HB2	11:AJ:43:ASN:HD22	1.86	0.41
11:AK:439:ILE:HD12	11:AK:439:ILE:HA	1.85	0.41
11:AL:230:LEU:HB2	11:AM:230:LEU:HD12	2.02	0.41
11:AL:348:LEU:HD21	11:AM:335:LEU:HB3	2.03	0.41
11:AM:192:PRO:O	11:AM:200:GLY:HA3	2.21	0.41
11:AN:297:ARG:HD2	11:AN:300:GLN:OE1	2.21	0.41
11:AN:469:THR:HG22	11:AN:479:VAL:HG22	2.02	0.41
11:AO:96:PRO:HB3	11:AO:107:TRP:CG	2.56	0.41
11:AR:205:ALA:HB3	11:AR:220:VAL:HA	2.02	0.41
11:AR:251:LEU:HD13	11:AR:255:ALA:HB1	2.03	0.41
11:AS:202:MET:HG2	11:AS:219:ALA:HB2	2.02	0.41
1:0:312:MET:HE2	1:0:320:VAL:HG12	2.03	0.41
3:C:173:SER:C	3:C:174:PHE:HD1	2.29	0.41
3:D:109:GLU:O	3:D:111:ILE:HG12	2.21	0.41
3:F:204:ARG:NE	6:m:14:ASP:HB3	2.36	0.41
1:L:337:PRO:HG2	1:L:368:VAL:HG11	2.02	0.41
4:Q:43:ILE:HG13	4:Q:44:ARG:HG3	2.03	0.41
1:W:161:LYS:H	1:W:228:ALA:HB2	1.86	0.41
1:W:165:ASP:HB2	1:W:168:ASN:OD1	2.21	0.41
1:X:231:LEU:HD23	1:X:231:LEU:HA	1.93	0.41
2:Y:237:ILE:HD13	2:Y:237:ILE:HA	1.92	0.41
2:i:176:LYS:NZ	2:i:177:ILE:HG22	2.36	0.41
8:j:60:PRO:HB2	9:d:170:GLN:HG3	2.03	0.41
2:p:147:VAL:HG22	2:p:197:PRO:HG2	2.03	0.41
2:v:62:LYS:HE3	2:v:62:LYS:HB3	1.93	0.41
5:x:143:GLN:C	5:x:145:LEU:H	2.29	0.41
9:J:241:ARG:HA	9:J:241:ARG:HD2	1.84	0.41
9:T:50:LYS:HD2	9:T:184:GLU:OE1	2.20	0.41
9:T:146:LEU:HD23	9:T:146:LEU:HA	1.92	0.41
9:d:63:LEU:HA	9:d:63:LEU:HD23	1.87	0.41
11:AE:483:TRP:CD1	11:AF:462:ILE:HG12	2.56	0.41
11:AB:216:ASP:OD1	11:AC:223:LEU:HB3	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:AC:391:VAL:HG12	11:AD:401:MET:HE2	2.03	0.41
11:AC:441:LEU:HD12	11:AC:475:THR:O	2.20	0.41
11:AD:356:ARG:HA	11:AD:356:ARG:HD3	1.90	0.41
11:AJ:30:LEU:HD13	11:AJ:30:LEU:HA	1.94	0.41
11:AK:98:ASP:OD2	11:AK:100:LEU:HB2	2.21	0.41
11:AK:482:ASN:CG	11:AK:483:TRP:N	2.79	0.41
11:AM:279:ARG:HB3	11:AM:284:ILE:HB	2.03	0.41
11:AN:69:GLU:HB3	11:AP:1:MET:HG3	2.02	0.41
11:AN:411:SER:HA	11:AN:427:THR:HG22	2.03	0.41
11:AO:137:ILE:HD12	11:AO:137:ILE:H	1.86	0.41
11:AP:234:ASP:HB3	11:AP:237:SER:OG	2.21	0.41
11:AQ:242:VAL:O	11:AQ:246:ARG:HG3	2.21	0.41
11:AR:159:TYR:HD1	11:AR:160:ALA:H	1.69	0.41
1:O:167:ILE:O	1:O:168:ASN:HB2	2.20	0.40
3:B:72:ASN:O	3:B:76:THR:HG23	2.20	0.40
3:D:90:VAL:HG13	3:D:127:GLN:HG2	2.03	0.40
1:L:379:ARG:HE	2:O:159:GLU:HA	1.86	0.40
1:L:397:ILE:HB	1:L:482:ILE:HA	2.03	0.40
2:O:88:PHE:HD1	2:O:88:PHE:HA	1.79	0.40
1:V:116:PRO:HB2	1:V:117:PRO:HD3	2.02	0.40
1:W:100:ARG:HE	1:W:241:ILE:HD11	1.86	0.40
1:X:252:GLN:HB2	1:X:276:ALA:HB3	2.02	0.40
7:e:59:LEU:HD13	7:e:59:LEU:HA	1.94	0.40
1:g:414:ILE:O	1:g:417:PRO:HD2	2.21	0.40
8:j:33:LEU:HD23	8:j:33:LEU:HA	1.94	0.40
7:n:2:ASP:HB3	7:n:31:GLN:HE22	1.86	0.40
2:p:87:GLY:HA2	2:p:108:PRO:O	2.21	0.40
2:p:107:ALA:HA	11:AK:36:LEU:CD1	2.51	0.40
5:x:18:HIS:NE2	5:x:73:ILE:HD12	2.36	0.40
5:x:18:HIS:CD2	5:x:73:ILE:HD12	2.57	0.40
11:AE:98:ASP:HA	11:AE:99:PRO:HD3	1.97	0.40
11:AE:152:LYS:HG2	11:AG:148:SER:OG	2.20	0.40
11:AE:249:LEU:HD13	11:AF:249:LEU:HD11	2.02	0.40
11:AF:390:ASP:O	11:AG:400:ALA:HB1	2.21	0.40
11:AB:319:GLY:CA	11:AC:325:PRO:HG3	2.51	0.40
11:AC:20:LYS:HE3	11:AC:47:TYR:CE1	2.56	0.40
11:AC:348:LEU:HD21	11:AD:335:LEU:HB3	2.03	0.40
11:AI:94:LYS:HD3	11:AI:94:LYS:HA	1.90	0.40
11:AI:159:TYR:HB2	11:AJ:161:MET:H	1.86	0.40
11:AL:81:ASN:OD1	11:AL:83:ILE:HG13	2.20	0.40
11:AP:455:MET:HG3	11:AP:489:PRO:HG2	2.03	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:AQ:308:LYS:O	11:AQ:312:ARG:HG3	2.21	0.40
11:AQ:319:GLY:O	11:AQ:323:THR:HG23	2.21	0.40
11:AR:434:ASP:HA	11:AS:458:PHE:HB2	2.03	0.40
1:O:298:VAL:HG23	1:O:299:GLN:H	1.86	0.40
3:E:141:ILE:HD13	3:E:141:ILE:HA	1.74	0.40
1:M:32:LEU:HB2	2:p:31:ARG:NH2	2.36	0.40
1:M:158:TYR:HE1	1:M:176:SER:HB2	1.87	0.40
1:M:249:PRO:HA	1:M:279:GLY:H	1.85	0.40
1:N:96:ALA:HB2	1:N:282:ARG:HG2	2.02	0.40
2:O:33:LEU:HD23	2:O:33:LEU:HA	1.76	0.40
2:O:112:VAL:HG22	11:AF:38:PRO:CB	2.51	0.40
8:P:241:THR:HG23	8:Z:231:HIS:O	2.22	0.40
1:W:66:GLN:HE21	1:W:70:ASN:ND2	2.19	0.40
1:W:208:GLN:HE21	1:W:213:PHE:HE2	1.70	0.40
1:W:464:MET:HE3	1:W:464:MET:HB3	1.96	0.40
1:X:94:HIS:CG	1:X:280:ARG:HH12	2.40	0.40
1:X:299:GLN:HB3	2:i:139:ARG:HH12	1.86	0.40
4:a:108:VAL:HA	4:a:127:ILE:HD13	2.03	0.40
1:f:469:ILE:HD12	1:f:469:ILE:HA	1.99	0.40
1:h:67:MET:HE3	1:h:67:MET:HB2	1.98	0.40
5:r:114:ARG:HD2	5:x:32:VAL:HG22	2.02	0.40
5:x:64:ILE:HD12	5:x:70:THR:HB	2.03	0.40
6:y:66:MET:HE1	6:y:76:PHE:HD2	1.84	0.40
9:d:278:VAL:HG12	9:d:280:ILE:HG13	2.03	0.40
11:AF:69:GLU:HG2	11:AF:91:HIS:O	2.21	0.40
11:AG:165:ASN:HB3	11:AG:168:ASN:CG	2.47	0.40
11:AB:160:ALA:HB3	11:AC:159:TYR:OH	2.21	0.40
11:AC:421:LEU:HA	11:AC:421:LEU:HD23	1.79	0.40
11:AD:260:SER:HA	11:AD:264:LYS:HE2	2.02	0.40
11:AD:401:MET:HE3	11:AD:403:PHE:HE1	1.85	0.40
11:AH:295:PHE:HD1	11:AH:295:PHE:HA	1.75	0.40
11:AH:308:LYS:H	11:AH:308:LYS:HG2	1.70	0.40
11:AI:13:ILE:HD11	11:AI:51:LEU:HA	2.03	0.40
11:AI:417:LEU:HD23	11:AI:417:LEU:HA	1.84	0.40
11:AK:422:LEU:HB3	11:AK:424:GLN:OE1	2.21	0.40
11:AL:20:LYS:HE3	11:AL:47:TYR:CE1	2.56	0.40
11:AM:471:MET:HE3	11:AM:471:MET:HB3	1.96	0.40
11:AN:329:MET:HB3	11:AO:329:MET:HA	2.04	0.40
11:AO:159:TYR:HB2	11:AP:160:ALA:H	1.87	0.40
11:AQ:210:THR:HG22	11:AQ:228:VAL:HG21	2.02	0.40
11:AR:246:ARG:HB3	11:AR:251:LEU:HG	2.02	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:AR:471:MET:O	11:AR:477:PHE:HA	2.21	0.40
11:AS:439:ILE:HD13	11:AS:439:ILE:HA	1.84	0.40
1:O:324:GLU:HG2	1:g:363:PHE:CE1	2.56	0.40
3:A:80:ASN:OD1	3:A:82:LYS:HB3	2.21	0.40
3:C:109:GLU:O	3:C:111:ILE:HG12	2.21	0.40
3:F:228:ASN:HD22	3:F:229:ALA:H	1.69	0.40
1:L:359:LEU:HD23	1:L:359:LEU:HA	1.92	0.40
1:L:415:LEU:HD23	1:L:415:LEU:HA	1.92	0.40
2:O:174:ILE:HG21	2:O:178:LEU:HD21	2.04	0.40
8:P:31:ARG:HE	8:P:31:ARG:HB2	1.75	0.40
4:Q:88:ILE:HD12	4:Q:88:ILE:HA	1.80	0.40
1:V:167:ILE:HD13	1:V:168:ASN:N	2.35	0.40
1:V:429:ILE:HA	1:V:474:VAL:HG23	2.04	0.40
2:Y:228:ASP:HB3	2:Y:231:ASP:HB3	2.02	0.40
1:f:104:VAL:HG22	1:f:239:LEU:HD23	2.04	0.40
1:f:158:TYR:CE1	1:f:176:SER:HB3	2.57	0.40
1:f:439:TYR:O	1:f:443:MET:HG2	2.21	0.40
1:g:253:GLN:HA	1:h:148:PHE:CE1	2.56	0.40
4:k:120:ILE:HD11	5:x:41:HIS:ND1	2.37	0.40
7:n:83:LEU:HD23	7:n:83:LEU:HA	1.87	0.40
2:p:145:GLU:O	2:p:149:GLU:HG2	2.22	0.40
2:v:33:LEU:HD23	2:v:33:LEU:HA	1.83	0.40
6:y:34:TRP:NE1	6:y:36:SER:HA	2.36	0.40
9:T:65:ILE:HD13	9:T:65:ILE:HA	1.94	0.40
11:AE:463:GLY:H	11:AG:483:TRP:CB	2.34	0.40
11:AF:173:ALA:HB2	11:AG:166:GLY:O	2.21	0.40
11:AB:87:CYS:HB2	11:AB:107:TRP:CZ3	2.56	0.40
11:AB:296:LEU:O	11:AD:296:LEU:HB2	2.22	0.40
11:AB:394:LEU:HD13	11:AB:394:LEU:HA	1.92	0.40
11:AD:116:GLU:O	11:AD:120:VAL:HG23	2.21	0.40
11:AH:380:ASN:ND2	11:AI:369:SER:HA	2.36	0.40
11:AI:35:GLU:HG2	11:AI:36:LEU:N	2.36	0.40
11:AK:89:ARG:HD2	11:AK:106:TYR:HE1	1.86	0.40
11:AL:352:THR:OG1	11:AM:358:THR:HG23	2.21	0.40
11:AM:449:ASN:HD21	11:AM:451:GLN:HE21	1.70	0.40
11:AQ:179:THR:O	11:AR:171:SER:HA	2.21	0.40
11:AR:413:GLY:HA3	11:AR:425:TRP:NE1	2.36	0.40
11:AS:122:ALA:HB1	11:AS:126:ARG:HH22	1.86	0.40
11:AS:282:LEU:HD23	11:AS:282:LEU:HA	1.90	0.40
1:O:447:GLY:H	1:N:437:ARG:HH12	1.68	0.40
3:D:21:PHE:HB3	3:F:176:GLU:OE1	2.22	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:429:ILE:HG22	1:L:474:VAL:HB	2.03	0.40
1:M:453:LEU:HD23	1:M:454:THR:N	2.37	0.40
1:N:474:VAL:HG22	1:N:475:ALA:O	2.21	0.40
2:O:83:PHE:O	2:O:91:THR:HG23	2.22	0.40
6:S:77:ASN:HB2	6:S:110:ASN:ND2	2.36	0.40
1:V:342:LEU:HD11	1:V:388:GLN:NE2	2.36	0.40
1:W:247:ILE:HD12	1:W:247:ILE:H	1.86	0.40
8:Z:172:LEU:HD23	8:j:180:SER:HB2	2.04	0.40
1:f:415:LEU:HA	1:f:415:LEU:HD23	1.89	0.40
1:g:177:PRO:HD2	1:g:182:VAL:HG22	2.02	0.40
1:g:429:ILE:HA	1:g:474:VAL:HB	2.02	0.40
8:j:111:ASN:HD22	8:j:111:ASN:HA	1.69	0.40
1:o:292:PHE:O	1:o:293:ARG:HB3	2.21	0.40
6:s:107:LEU:HD23	6:s:107:LEU:HA	1.91	0.40
2:v:126:GLU:HB3	2:v:185:LEU:HD21	2.02	0.40
2:v:176:LYS:HZ1	2:v:177:ILE:HG22	1.86	0.40
9:J:99:GLU:HG2	9:J:100:THR:N	2.36	0.40
9:J:238:LYS:HD2	9:J:238:LYS:HA	1.93	0.40
9:d:179:LEU:HD23	9:d:179:LEU:HA	1.94	0.40
11:AE:59:HIS:CE1	11:AF:3:ASN:HD21	2.40	0.40
11:AE:411:SER:HA	11:AE:427:THR:HG22	2.03	0.40
11:AF:150:TYR:CE1	11:AG:152:LYS:HA	2.57	0.40
11:AF:317:LEU:H	11:AF:317:LEU:HG	1.76	0.40
11:AG:297:ARG:NH2	11:AG:300:GLN:HG3	2.37	0.40
11:AB:58:GLN:NE2	11:AC:3:ASN:HA	2.32	0.40
11:AB:295:PHE:HD1	11:AB:295:PHE:HA	1.70	0.40
11:AB:343:THR:HG22	11:AB:347:ASN:ND2	2.36	0.40
11:AH:85:TYR:C	11:AH:110:ALA:HB2	2.46	0.40
11:AH:331:LYS:O	11:AH:331:LYS:HD3	2.21	0.40
11:AH:401:MET:HB2	11:AJ:391:VAL:HG12	2.04	0.40
11:AI:52:PHE:HD1	11:AJ:7:PRO:HD2	1.87	0.40
11:AK:449:ASN:ND2	11:AL:491:ASN:HB2	2.36	0.40
11:AM:422:LEU:HD23	11:AM:422:LEU:HA	1.83	0.40
11:AO:141:VAL:O	11:AO:145:GLN:HG3	2.21	0.40
11:AO:390:ASP:O	11:AP:400:ALA:HB1	2.21	0.40
11:AQ:279:ARG:HG3	11:AS:282:LEU:HD22	2.02	0.40
11:AR:91:HIS:CD2	11:AR:106:TYR:HD2	2.40	0.40
11:AR:413:GLY:HA3	11:AR:425:TRP:HE1	1.86	0.40
11:AR:446:ARG:HG2	11:AR:497:SER:O	2.21	0.40
3:C:140:LEU:HA	3:C:140:LEU:HD23	1.89	0.40
3:F:141:ILE:HD13	3:F:141:ILE:HA	1.72	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:M:366:GLY:N	1:o:326:ASP:HB2	2.37	0.40
8:P:219:SER:O	8:P:225:PRO:HA	2.22	0.40
5:R:33:LYS:HG3	5:R:58:TRP:CE2	2.56	0.40
5:R:33:LYS:HG3	5:R:58:TRP:CZ2	2.57	0.40
1:V:35:THR:HA	6:y:102:GLN:OE1	2.21	0.40
1:V:117:PRO:O	1:V:262:ILE:HG12	2.22	0.40
1:V:142:CYS:HB2	1:V:237:ARG:O	2.20	0.40
1:V:379:ARG:NH2	2:Y:160:VAL:HG12	2.36	0.40
1:W:91:ILE:HD13	1:W:91:ILE:HA	1.92	0.40
1:X:299:GLN:H	2:i:139:ARG:CZ	2.35	0.40
1:X:300:ALA:H	2:i:139:ARG:HH12	1.68	0.40
2:Y:176:LYS:HD2	2:Y:176:LYS:HA	1.93	0.40
5:b:68:SER:HA	5:b:69:PRO:HD3	1.95	0.40
7:e:85:ILE:HG13	7:e:105:VAL:HG12	2.04	0.40
1:g:13:ASP:O	1:g:17:ILE:HG13	2.22	0.40
1:g:162:MET:HG2	1:g:164:VAL:HG13	2.03	0.40
1:g:299:GLN:O	1:g:301:THR:HG23	2.22	0.40
8:j:202:TRP:CE2	8:j:206:ILE:HD11	2.57	0.40
6:m:34:TRP:HE1	6:m:36:SER:HA	1.87	0.40
1:o:167:ILE:C	1:o:169:THR:H	2.29	0.40
2:p:84:ASN:HA	2:p:91:THR:H	1.87	0.40
4:q:60:ARG:HG2	4:q:126:THR:HG22	2.03	0.40
9:J:66:ALA:O	9:J:70:ILE:HG22	2.21	0.40
11:AE:38:PRO:HG2	11:AE:41:THR:OG1	2.21	0.40
11:AF:96:PRO:HB3	11:AF:107:TRP:CG	2.57	0.40
11:AG:1:MET:HE2	11:AG:1:MET:HB3	2.00	0.40
11:AG:417:LEU:HA	11:AG:417:LEU:HD23	1.84	0.40
11:AB:175:ALA:HB3	11:AB:186:GLN:HE22	1.86	0.40
11:AB:309:ALA:HA	11:AB:312:ARG:HE	1.87	0.40
11:AB:350:LEU:HD21	11:AC:350:LEU:HD13	2.04	0.40
11:AC:282:LEU:O	11:AD:279:ARG:HD3	2.22	0.40
11:AC:389:LEU:HD22	11:AD:400:ALA:HA	2.03	0.40
11:AC:459:ASN:HB3	11:AC:488:TYR:OH	2.22	0.40
11:AJ:300:GLN:HG2	11:AJ:303:ALA:HB3	2.03	0.40
11:AN:89:ARG:HD2	11:AN:106:TYR:CE1	2.56	0.40
11:AN:298:SER:HB3	11:AP:304:ASP:CG	2.46	0.40

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	0	484/487 (99%)	456 (94%)	28 (6%)	0	100	100
1	L	484/487 (99%)	460 (95%)	24 (5%)	0	100	100
1	M	484/487 (99%)	450 (93%)	32 (7%)	2 (0%)	30	66
1	N	484/487 (99%)	460 (95%)	23 (5%)	1 (0%)	43	77
1	V	484/487 (99%)	460 (95%)	24 (5%)	0	100	100
1	W	484/487 (99%)	450 (93%)	34 (7%)	0	100	100
1	X	484/487 (99%)	460 (95%)	23 (5%)	1 (0%)	43	77
1	f	484/487 (99%)	459 (95%)	25 (5%)	0	100	100
1	g	484/487 (99%)	456 (94%)	28 (6%)	0	100	100
1	h	484/487 (99%)	457 (94%)	26 (5%)	1 (0%)	43	77
1	o	484/487 (99%)	459 (95%)	25 (5%)	0	100	100
1	u	484/487 (99%)	463 (96%)	21 (4%)	0	100	100
2	1	240/243 (99%)	216 (90%)	23 (10%)	1 (0%)	30	66
2	O	240/243 (99%)	219 (91%)	20 (8%)	1 (0%)	30	66
2	Y	240/243 (99%)	215 (90%)	24 (10%)	1 (0%)	30	66
2	i	240/243 (99%)	215 (90%)	24 (10%)	1 (0%)	30	66
2	p	240/243 (99%)	216 (90%)	23 (10%)	1 (0%)	30	66
2	v	240/243 (99%)	215 (90%)	24 (10%)	1 (0%)	30	66
3	A	235/253 (93%)	209 (89%)	26 (11%)	0	100	100
3	B	235/253 (93%)	209 (89%)	26 (11%)	0	100	100
3	C	235/253 (93%)	206 (88%)	29 (12%)	0	100	100
3	D	235/253 (93%)	207 (88%)	28 (12%)	0	100	100
3	E	235/253 (93%)	211 (90%)	24 (10%)	0	100	100
3	F	235/253 (93%)	212 (90%)	23 (10%)	0	100	100
4	G	156/159 (98%)	145 (93%)	11 (7%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
4	Q	156/159 (98%)	148 (95%)	8 (5%)	0	100	100
4	a	156/159 (98%)	142 (91%)	14 (9%)	0	100	100
4	k	156/159 (98%)	150 (96%)	6 (4%)	0	100	100
4	q	156/159 (98%)	143 (92%)	13 (8%)	0	100	100
4	w	156/159 (98%)	147 (94%)	9 (6%)	0	100	100
5	H	164/166 (99%)	156 (95%)	8 (5%)	0	100	100
5	R	164/166 (99%)	153 (93%)	11 (7%)	0	100	100
5	b	164/166 (99%)	157 (96%)	7 (4%)	0	100	100
5	l	164/166 (99%)	156 (95%)	8 (5%)	0	100	100
5	r	164/166 (99%)	153 (93%)	11 (7%)	0	100	100
5	x	164/166 (99%)	154 (94%)	10 (6%)	0	100	100
6	I	112/117 (96%)	105 (94%)	7 (6%)	0	100	100
6	S	112/117 (96%)	105 (94%)	7 (6%)	0	100	100
6	c	112/117 (96%)	107 (96%)	5 (4%)	0	100	100
6	m	112/117 (96%)	105 (94%)	7 (6%)	0	100	100
6	s	112/117 (96%)	108 (96%)	4 (4%)	0	100	100
6	y	112/117 (96%)	104 (93%)	8 (7%)	0	100	100
7	K	118/123 (96%)	105 (89%)	13 (11%)	0	100	100
7	U	118/123 (96%)	111 (94%)	7 (6%)	0	100	100
7	e	118/123 (96%)	112 (95%)	6 (5%)	0	100	100
7	n	118/123 (96%)	103 (87%)	15 (13%)	0	100	100
7	t	118/123 (96%)	112 (95%)	6 (5%)	0	100	100
7	z	118/123 (96%)	102 (86%)	16 (14%)	0	100	100
8	P	244/246 (99%)	233 (96%)	10 (4%)	1 (0%)	30	66
8	Z	244/246 (99%)	230 (94%)	14 (6%)	0	100	100
8	j	244/246 (99%)	236 (97%)	7 (3%)	1 (0%)	30	66
9	J	302/305 (99%)	271 (90%)	31 (10%)	0	100	100
9	T	302/305 (99%)	273 (90%)	29 (10%)	0	100	100
9	d	302/305 (99%)	273 (90%)	29 (10%)	0	100	100
10	2	17/788 (2%)	17 (100%)	0	0	100	100
10	3	17/788 (2%)	17 (100%)	0	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
10	4	17/788 (2%)	17 (100%)	0	0	100	100
10	5	17/788 (2%)	17 (100%)	0	0	100	100
10	6	17/788 (2%)	17 (100%)	0	0	100	100
10	7	17/788 (2%)	17 (100%)	0	0	100	100
10	8	30/788 (4%)	28 (93%)	2 (7%)	0	100	100
10	9	30/788 (4%)	29 (97%)	1 (3%)	0	100	100
10	AA	30/788 (4%)	28 (93%)	2 (7%)	0	100	100
11	AB	497/499 (100%)	476 (96%)	21 (4%)	0	100	100
11	AC	497/499 (100%)	464 (93%)	33 (7%)	0	100	100
11	AD	497/499 (100%)	465 (94%)	32 (6%)	0	100	100
11	AE	497/499 (100%)	478 (96%)	19 (4%)	0	100	100
11	AF	497/499 (100%)	468 (94%)	29 (6%)	0	100	100
11	AG	497/499 (100%)	469 (94%)	28 (6%)	0	100	100
11	AH	497/499 (100%)	481 (97%)	16 (3%)	0	100	100
11	AI	497/499 (100%)	466 (94%)	31 (6%)	0	100	100
11	AJ	497/499 (100%)	466 (94%)	31 (6%)	0	100	100
11	AK	497/499 (100%)	478 (96%)	19 (4%)	0	100	100
11	AL	497/499 (100%)	470 (95%)	27 (5%)	0	100	100
11	AM	497/499 (100%)	470 (95%)	27 (5%)	0	100	100
11	AN	497/499 (100%)	476 (96%)	21 (4%)	0	100	100
11	AO	497/499 (100%)	464 (93%)	33 (7%)	0	100	100
11	AP	497/499 (100%)	468 (94%)	29 (6%)	0	100	100
11	AQ	497/499 (100%)	479 (96%)	18 (4%)	0	100	100
11	AR	497/499 (100%)	470 (95%)	27 (5%)	0	100	100
11	AS	497/499 (100%)	473 (95%)	24 (5%)	0	100	100
All	All	22734/29937 (76%)	21307 (94%)	1414 (6%)	13 (0%)	49	82

All (13) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	1	118	ASN
1	M	285	ASP
2	O	118	ASN

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Mol	Chain	Res	Type
2	Y	118	ASN
2	i	118	ASN
2	p	118	ASN
2	v	118	ASN
8	P	4	THR
8	j	6	LEU
1	M	167	ILE
1	X	167	ILE
1	h	167	ILE
1	N	167	ILE

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	0	410/411 (100%)	383 (93%)	27 (7%)	15	38
1	L	410/411 (100%)	377 (92%)	33 (8%)	11	32
1	M	410/411 (100%)	380 (93%)	30 (7%)	13	35
1	N	410/411 (100%)	384 (94%)	26 (6%)	16	39
1	V	410/411 (100%)	378 (92%)	32 (8%)	11	33
1	W	410/411 (100%)	386 (94%)	24 (6%)	18	41
1	X	410/411 (100%)	388 (95%)	22 (5%)	20	43
1	f	410/411 (100%)	380 (93%)	30 (7%)	13	35
1	g	410/411 (100%)	382 (93%)	28 (7%)	14	37
1	h	410/411 (100%)	385 (94%)	25 (6%)	17	40
1	o	410/411 (100%)	385 (94%)	25 (6%)	17	40
1	u	410/411 (100%)	380 (93%)	30 (7%)	13	35
2	1	197/198 (100%)	172 (87%)	25 (13%)	4	18
2	O	197/198 (100%)	179 (91%)	18 (9%)	9	29
2	Y	197/198 (100%)	170 (86%)	27 (14%)	3	16
2	i	197/198 (100%)	180 (91%)	17 (9%)	10	30

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	p	197/198 (100%)	170 (86%)	27 (14%)	3	16
2	v	197/198 (100%)	175 (89%)	22 (11%)	6	21
3	A	212/226 (94%)	193 (91%)	19 (9%)	9	29
3	B	212/226 (94%)	187 (88%)	25 (12%)	5	20
3	C	212/226 (94%)	193 (91%)	19 (9%)	9	29
3	D	212/226 (94%)	186 (88%)	26 (12%)	4	19
3	E	212/226 (94%)	186 (88%)	26 (12%)	4	19
3	F	212/226 (94%)	191 (90%)	21 (10%)	7	25
4	G	138/139 (99%)	125 (91%)	13 (9%)	8	27
4	Q	138/139 (99%)	120 (87%)	18 (13%)	4	17
4	a	138/139 (99%)	127 (92%)	11 (8%)	11	32
4	k	138/139 (99%)	125 (91%)	13 (9%)	8	27
4	q	138/139 (99%)	126 (91%)	12 (9%)	9	30
4	w	138/139 (99%)	126 (91%)	12 (9%)	9	30
5	H	142/142 (100%)	130 (92%)	12 (8%)	10	30
5	R	142/142 (100%)	133 (94%)	9 (6%)	16	39
5	b	142/142 (100%)	132 (93%)	10 (7%)	14	37
5	l	142/142 (100%)	133 (94%)	9 (6%)	16	39
5	r	142/142 (100%)	132 (93%)	10 (7%)	14	37
5	x	142/142 (100%)	135 (95%)	7 (5%)	22	45
6	I	104/107 (97%)	97 (93%)	7 (7%)	15	37
6	S	104/107 (97%)	97 (93%)	7 (7%)	15	37
6	c	104/107 (97%)	94 (90%)	10 (10%)	8	26
6	m	104/107 (97%)	96 (92%)	8 (8%)	12	33
6	s	104/107 (97%)	95 (91%)	9 (9%)	9	30
6	y	104/107 (97%)	95 (91%)	9 (9%)	9	30
7	K	110/112 (98%)	104 (94%)	6 (6%)	19	43
7	U	110/112 (98%)	101 (92%)	9 (8%)	10	32
7	e	110/112 (98%)	100 (91%)	10 (9%)	9	29
7	n	110/112 (98%)	103 (94%)	7 (6%)	16	38
7	t	110/112 (98%)	102 (93%)	8 (7%)	13	35

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
7	z	110/112 (98%)	102 (93%)	8 (7%)	13	35
8	P	209/209 (100%)	201 (96%)	8 (4%)	29	51
8	Z	209/209 (100%)	191 (91%)	18 (9%)	10	30
8	j	209/209 (100%)	193 (92%)	16 (8%)	12	33
9	J	265/266 (100%)	232 (88%)	33 (12%)	4	18
9	T	265/266 (100%)	231 (87%)	34 (13%)	4	18
9	d	265/266 (100%)	236 (89%)	29 (11%)	6	22
10	2	15/620 (2%)	15 (100%)	0	100	100
10	3	15/620 (2%)	15 (100%)	0	100	100
10	4	15/620 (2%)	15 (100%)	0	100	100
10	5	15/620 (2%)	14 (93%)	1 (7%)	15	37
10	6	15/620 (2%)	15 (100%)	0	100	100
10	7	15/620 (2%)	15 (100%)	0	100	100
10	8	29/620 (5%)	28 (97%)	1 (3%)	32	55
10	9	29/620 (5%)	23 (79%)	6 (21%)	1	7
10	AA	29/620 (5%)	24 (83%)	5 (17%)	2	12
11	AB	398/398 (100%)	368 (92%)	30 (8%)	12	34
11	AC	398/398 (100%)	369 (93%)	29 (7%)	13	35
11	AD	398/398 (100%)	367 (92%)	31 (8%)	11	33
11	AE	398/398 (100%)	365 (92%)	33 (8%)	10	31
11	AF	398/398 (100%)	360 (90%)	38 (10%)	8	26
11	AG	398/398 (100%)	364 (92%)	34 (8%)	10	30
11	AH	398/398 (100%)	365 (92%)	33 (8%)	10	31
11	AI	398/398 (100%)	362 (91%)	36 (9%)	9	29
11	AJ	398/398 (100%)	363 (91%)	35 (9%)	9	30
11	AK	398/398 (100%)	366 (92%)	32 (8%)	11	32
11	AL	398/398 (100%)	371 (93%)	27 (7%)	14	37
11	AM	398/398 (100%)	362 (91%)	36 (9%)	9	29
11	AN	398/398 (100%)	372 (94%)	26 (6%)	15	38
11	AO	398/398 (100%)	358 (90%)	40 (10%)	7	24
11	AP	398/398 (100%)	365 (92%)	33 (8%)	10	31

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
11	AQ	398/398 (100%)	366 (92%)	32 (8%)	11	32
11	AR	398/398 (100%)	368 (92%)	30 (8%)	12	34
11	AS	398/398 (100%)	370 (93%)	28 (7%)	14	37
All	All	19101/24645 (78%)	17529 (92%)	1572 (8%)	13	32

All (1572) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	0	11	ILE
1	0	15	ASP
1	0	72	PHE
1	0	109	ILE
1	0	130	HIS
1	0	140	LYS
1	0	145	VAL
1	0	147	ILE
1	0	159	GLU
1	0	167	ILE
1	0	172	ILE
1	0	234	GLN
1	0	257	ILE
1	0	262	ILE
1	0	274	VAL
1	0	291	ARG
1	0	293	ARG
1	0	298	VAL
1	0	299	GLN
1	0	351	THR
1	0	355	GLN
1	0	373	VAL
1	0	376	VAL
1	0	413	ASP
1	0	428	LYS
1	0	442	ILE
1	0	469	ILE
2	1	20	THR
2	1	31	ARG
2	1	32	PHE
2	1	33	LEU
2	1	35	VAL
2	1	44	GLN

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Mol	Chain	Res	Type
2	1	53	LEU
2	1	62	LYS
2	1	77	LEU
2	1	88	PHE
2	1	91	THR
2	1	92	GLU
2	1	93	ARG
2	1	109	TRP
2	1	112	VAL
2	1	126	GLU
2	1	139	ARG
2	1	160	VAL
2	1	162	LEU
2	1	165	TYR
2	1	200	ILE
2	1	208	GLU
2	1	214	VAL
2	1	217	THR
2	1	238	LEU
3	A	6	LYS
3	A	29	VAL
3	A	31	SER
3	A	44	ILE
3	A	57	VAL
3	A	65	ASN
3	A	69	ILE
3	A	75	GLN
3	A	82	LYS
3	A	85	VAL
3	A	86	ASN
3	A	87	THR
3	A	105	ARG
3	A	114	PHE
3	A	118	GLU
3	A	127	GLN
3	A	199	ARG
3	A	211	THR
3	A	217	ARG
3	B	5	ILE
3	B	24	GLN
3	B	46	THR
3	B	62	PHE

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Mol	Chain	Res	Type
3	B	63	ASN
3	B	87	THR
3	B	98	THR
3	B	110	VAL
3	B	114	PHE
3	B	124	VAL
3	B	128	LYS
3	B	131	LYS
3	B	176	GLU
3	B	177	ASN
3	B	199	ARG
3	B	205	VAL
3	B	207	LYS
3	B	210	LYS
3	B	214	LYS
3	B	216	LYS
3	B	217	ARG
3	B	224	THR
3	B	230	THR
3	B	234	SER
3	B	238	LYS
3	C	6	LYS
3	C	29	VAL
3	C	31	SER
3	C	44	ILE
3	C	65	ASN
3	C	69	ILE
3	C	82	LYS
3	C	85	VAL
3	C	87	THR
3	C	105	ARG
3	C	114	PHE
3	C	118	GLU
3	C	144	GLN
3	C	174	PHE
3	C	199	ARG
3	C	207	LYS
3	C	211	THR
3	C	217	ARG
3	C	230	THR
3	D	2	THR
3	D	6	LYS

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Mol	Chain	Res	Type
3	D	31	SER
3	D	35	GLU
3	D	44	ILE
3	D	57	VAL
3	D	65	ASN
3	D	69	ILE
3	D	73	GLU
3	D	82	LYS
3	D	85	VAL
3	D	87	THR
3	D	90	VAL
3	D	96	ILE
3	D	105	ARG
3	D	114	PHE
3	D	118	GLU
3	D	127	GLN
3	D	144	GLN
3	D	199	ARG
3	D	202	GLU
3	D	207	LYS
3	D	211	THR
3	D	217	ARG
3	D	224	THR
3	D	234	SER
3	E	5	ILE
3	E	24	GLN
3	E	40	ILE
3	E	46	THR
3	E	62	PHE
3	E	63	ASN
3	E	82	LYS
3	E	87	THR
3	E	90	VAL
3	E	98	THR
3	E	110	VAL
3	E	114	PHE
3	E	128	LYS
3	E	141	ILE
3	E	168	ILE
3	E	176	GLU
3	E	177	ASN
3	E	199	ARG

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Mol	Chain	Res	Type
3	E	205	VAL
3	E	210	LYS
3	E	214	LYS
3	E	217	ARG
3	E	224	THR
3	E	228	ASN
3	E	230	THR
3	E	234	SER
3	F	36	THR
3	F	80	ASN
3	F	87	THR
3	F	98	THR
3	F	110	VAL
3	F	114	PHE
3	F	131	LYS
3	F	141	ILE
3	F	142	ASP
3	F	176	GLU
3	F	177	ASN
3	F	199	ARG
3	F	205	VAL
3	F	210	LYS
3	F	217	ARG
3	F	221	GLU
3	F	224	THR
3	F	228	ASN
3	F	230	THR
3	F	234	SER
3	F	238	LYS
4	G	33	LEU
4	G	35	ARG
4	G	68	VAL
4	G	96	HIS
4	G	100	MET
4	G	103	THR
4	G	111	TYR
4	G	120	ILE
4	G	121	GLU
4	G	126	THR
4	G	143	VAL
4	G	150	THR
4	G	151	VAL

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Mol	Chain	Res	Type
5	H	4	THR
5	H	8	ARG
5	H	11	VAL
5	H	13	THR
5	H	34	ASP
5	H	40	LYS
5	H	62	LEU
5	H	77	LEU
5	H	80	VAL
5	H	82	ILE
5	H	96	THR
5	H	133	VAL
6	I	8	THR
6	I	18	ARG
6	I	23	ILE
6	I	26	ILE
6	I	44	ASP
6	I	48	GLU
6	I	68	ASP
7	K	15	ILE
7	K	26	VAL
7	K	38	TYR
7	K	82	VAL
7	K	92	ILE
7	K	108	THR
1	L	11	ILE
1	L	28	VAL
1	L	29	PHE
1	L	45	SER
1	L	65	ILE
1	L	85	LEU
1	L	109	ILE
1	L	120	MET
1	L	128	VAL
1	L	130	HIS
1	L	159	GLU
1	L	169	THR
1	L	170	THR
1	L	172	ILE
1	L	191	LEU
1	L	234	GLN
1	L	257	ILE

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Mol	Chain	Res	Type
1	L	271	ILE
1	L	288	LEU
1	L	290	GLU
1	L	293	ARG
1	L	303	ILE
1	L	336	VAL
1	L	372	GLU
1	L	384	ARG
1	L	399	ILE
1	L	406	SER
1	L	410	ASN
1	L	428	LYS
1	L	435	TYR
1	L	449	GLN
1	L	464	MET
1	L	468	GLU
1	M	5	THR
1	M	37	ASP
1	M	50	LEU
1	M	84	ASN
1	M	91	ILE
1	M	105	LEU
1	M	140	LYS
1	M	147	ILE
1	M	165	ASP
1	M	167	ILE
1	M	181	THR
1	M	203	LEU
1	M	213	PHE
1	M	241	ILE
1	M	253	GLN
1	M	259	THR
1	M	270	VAL
1	M	283	GLU
1	M	285	ASP
1	M	289	ARG
1	M	293	ARG
1	M	296	LYS
1	M	298	VAL
1	M	329	ASN
1	M	376	VAL
1	M	393	VAL

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Mol	Chain	Res	Type
1	M	401	VAL
1	M	402	THR
1	M	439	TYR
1	M	458	LYS
1	N	5	THR
1	N	32	LEU
1	N	39	VAL
1	N	50	LEU
1	N	85	LEU
1	N	86	VAL
1	N	115	SER
1	N	157	THR
1	N	182	VAL
1	N	204	THR
1	N	213	PHE
1	N	222	THR
1	N	234	GLN
1	N	236	VAL
1	N	270	VAL
1	N	303	ILE
1	N	333	VAL
1	N	359	LEU
1	N	374	GLN
1	N	382	THR
1	N	393	VAL
1	N	401	VAL
1	N	407	MET
1	N	437	ARG
1	N	443	MET
1	N	445	ILE
2	O	33	LEU
2	O	66	ILE
2	O	77	LEU
2	O	78	VAL
2	O	88	PHE
2	O	93	ARG
2	O	123	SER
2	O	136	ILE
2	O	139	ARG
2	O	145	GLU
2	O	163	GLU
2	O	170	VAL

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Mol	Chain	Res	Type
2	O	176	LYS
2	O	208	GLU
2	O	214	VAL
2	O	217	THR
2	O	238	LEU
2	O	239	THR
8	P	1	MET
8	P	12	LEU
8	P	28	VAL
8	P	81	LEU
8	P	117	ASN
8	P	129	THR
8	P	148	ASP
8	P	208	HIS
4	Q	26	VAL
4	Q	35	ARG
4	Q	39	MET
4	Q	53	ARG
4	Q	75	SER
4	Q	78	GLU
4	Q	79	GLN
4	Q	88	ILE
4	Q	92	VAL
4	Q	96	HIS
4	Q	100	MET
4	Q	120	ILE
4	Q	122	ASN
4	Q	123	ARG
4	Q	134	ASP
4	Q	143	VAL
4	Q	150	THR
4	Q	158	LEU
5	R	8	ARG
5	R	11	VAL
5	R	25	GLU
5	R	34	ASP
5	R	47	GLU
5	R	51	VAL
5	R	80	VAL
5	R	82	ILE
5	R	91	LEU
6	S	15	ARG

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Mol	Chain	Res	Type
6	S	17	TYR
6	S	19	TYR
6	S	23	ILE
6	S	26	ILE
6	S	53	ILE
6	S	113	LEU
7	U	11	ASP
7	U	15	ILE
7	U	26	VAL
7	U	65	LEU
7	U	72	PHE
7	U	92	ILE
7	U	99	TYR
7	U	108	THR
7	U	114	LEU
1	V	15	ASP
1	V	68	VAL
1	V	109	ILE
1	V	130	HIS
1	V	140	LYS
1	V	145	VAL
1	V	147	ILE
1	V	159	GLU
1	V	167	ILE
1	V	172	ILE
1	V	202	THR
1	V	213	PHE
1	V	218	ASP
1	V	257	ILE
1	V	262	ILE
1	V	274	VAL
1	V	293	ARG
1	V	296	LYS
1	V	298	VAL
1	V	303	ILE
1	V	324	GLU
1	V	325	ASN
1	V	327	THR
1	V	351	THR
1	V	355	GLN
1	V	373	VAL
1	V	413	ASP

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Mol	Chain	Res	Type
1	V	428	LYS
1	V	442	ILE
1	V	464	MET
1	V	468	GLU
1	V	469	ILE
1	W	21	TYR
1	W	32	LEU
1	W	37	ASP
1	W	73	ASN
1	W	84	ASN
1	W	93	ARG
1	W	105	LEU
1	W	128	VAL
1	W	147	ILE
1	W	165	ASP
1	W	170	THR
1	W	181	THR
1	W	203	LEU
1	W	213	PHE
1	W	241	ILE
1	W	259	THR
1	W	296	LYS
1	W	298	VAL
1	W	329	ASN
1	W	370	ASP
1	W	393	VAL
1	W	401	VAL
1	W	439	TYR
1	W	458	LYS
1	X	5	THR
1	X	32	LEU
1	X	49	ARG
1	X	85	LEU
1	X	86	VAL
1	X	115	SER
1	X	157	THR
1	X	182	VAL
1	X	204	THR
1	X	213	PHE
1	X	222	THR
1	X	234	GLN
1	X	270	VAL

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Mol	Chain	Res	Type
1	X	303	ILE
1	X	333	VAL
1	X	374	GLN
1	X	382	THR
1	X	393	VAL
1	X	415	LEU
1	X	437	ARG
1	X	445	ILE
1	X	450	VAL
2	Y	20	THR
2	Y	22	GLN
2	Y	32	PHE
2	Y	33	LEU
2	Y	35	VAL
2	Y	44	GLN
2	Y	47	LEU
2	Y	53	LEU
2	Y	58	THR
2	Y	77	LEU
2	Y	88	PHE
2	Y	91	THR
2	Y	92	GLU
2	Y	93	ARG
2	Y	109	TRP
2	Y	112	VAL
2	Y	118	ASN
2	Y	136	ILE
2	Y	138	ASN
2	Y	139	ARG
2	Y	160	VAL
2	Y	162	LEU
2	Y	165	TYR
2	Y	180	ASN
2	Y	200	ILE
2	Y	214	VAL
2	Y	217	THR
8	Z	1	MET
8	Z	2	ARG
8	Z	6	LEU
8	Z	12	LEU
8	Z	25	ILE
8	Z	28	VAL

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Mol	Chain	Res	Type
8	Z	81	LEU
8	Z	82	ASN
8	Z	98	VAL
8	Z	112	ASP
8	Z	136	ASP
8	Z	148	ASP
8	Z	177	LYS
8	Z	208	HIS
8	Z	221	PHE
8	Z	227	HIS
8	Z	230	LYS
8	Z	245	GLN
4	a	22	LEU
4	a	35	ARG
4	a	79	GLN
4	a	96	HIS
4	a	100	MET
4	a	103	THR
4	a	111	TYR
4	a	120	ILE
4	a	143	VAL
4	a	150	THR
4	a	151	VAL
5	b	4	THR
5	b	13	THR
5	b	70	THR
5	b	77	LEU
5	b	80	VAL
5	b	82	ILE
5	b	96	THR
5	b	125	THR
5	b	133	VAL
5	b	148	GLN
6	c	3	THR
6	c	8	THR
6	c	18	ARG
6	c	23	ILE
6	c	44	ASP
6	c	48	GLU
6	c	54	LEU
6	c	59	VAL
6	c	68	ASP

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Mol	Chain	Res	Type
6	c	83	MET
7	e	11	ASP
7	e	12	LEU
7	e	15	ILE
7	e	26	VAL
7	e	65	LEU
7	e	72	PHE
7	e	92	ILE
7	e	99	TYR
7	e	108	THR
7	e	114	LEU
1	f	21	TYR
1	f	29	PHE
1	f	33	VAL
1	f	39	VAL
1	f	45	SER
1	f	65	ILE
1	f	78	THR
1	f	85	LEU
1	f	128	VAL
1	f	130	HIS
1	f	159	GLU
1	f	169	THR
1	f	179	THR
1	f	191	LEU
1	f	194	ASP
1	f	218	ASP
1	f	234	GLN
1	f	257	ILE
1	f	271	ILE
1	f	288	LEU
1	f	290	GLU
1	f	293	ARG
1	f	298	VAL
1	f	325	ASN
1	f	410	ASN
1	f	428	LYS
1	f	434	ILE
1	f	435	TYR
1	f	449	GLN
1	f	468	GLU
1	g	29	PHE

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Mol	Chain	Res	Type
1	g	32	LEU
1	g	37	ASP
1	g	50	LEU
1	g	84	ASN
1	g	105	LEU
1	g	147	ILE
1	g	170	THR
1	g	181	THR
1	g	203	LEU
1	g	213	PHE
1	g	241	ILE
1	g	247	ILE
1	g	259	THR
1	g	270	VAL
1	g	281	LEU
1	g	283	GLU
1	g	296	LYS
1	g	298	VAL
1	g	302	ASN
1	g	329	ASN
1	g	360	ASN
1	g	376	VAL
1	g	393	VAL
1	g	401	VAL
1	g	439	TYR
1	g	458	LYS
1	g	487	VAL
1	h	5	THR
1	h	32	LEU
1	h	37	ASP
1	h	49	ARG
1	h	85	LEU
1	h	86	VAL
1	h	115	SER
1	h	157	THR
1	h	172	ILE
1	h	182	VAL
1	h	204	THR
1	h	213	PHE
1	h	222	THR
1	h	234	GLN
1	h	236	VAL

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Mol	Chain	Res	Type
1	h	270	VAL
1	h	302	ASN
1	h	303	ILE
1	h	333	VAL
1	h	374	GLN
1	h	382	THR
1	h	393	VAL
1	h	437	ARG
1	h	443	MET
1	h	445	ILE
2	i	33	LEU
2	i	54	ARG
2	i	56	LEU
2	i	66	ILE
2	i	67	ILE
2	i	77	LEU
2	i	91	THR
2	i	93	ARG
2	i	136	ILE
2	i	145	GLU
2	i	152	LYS
2	i	163	GLU
2	i	170	VAL
2	i	176	LYS
2	i	214	VAL
2	i	217	THR
2	i	239	THR
8	j	1	MET
8	j	2	ARG
8	j	3	ARG
8	j	8	GLU
8	j	25	ILE
8	j	28	VAL
8	j	111	ASN
8	j	112	ASP
8	j	117	ASN
8	j	136	ASP
8	j	148	ASP
8	j	156	MET
8	j	157	THR
8	j	208	HIS
8	j	230	LYS

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Mol	Chain	Res	Type
8	j	245	GLN
4	k	35	ARG
4	k	53	ARG
4	k	68	VAL
4	k	75	SER
4	k	78	GLU
4	k	79	GLN
4	k	96	HIS
4	k	120	ILE
4	k	122	ASN
4	k	123	ARG
4	k	143	VAL
4	k	150	THR
4	k	151	VAL
5	l	11	VAL
5	l	25	GLU
5	l	47	GLU
5	l	53	ASN
5	l	79	ASN
5	l	80	VAL
5	l	82	ILE
5	l	96	THR
5	l	133	VAL
6	m	3	THR
6	m	17	TYR
6	m	19	TYR
6	m	23	ILE
6	m	26	ILE
6	m	53	ILE
6	m	65	ILE
6	m	113	LEU
7	n	26	VAL
7	n	29	VAL
7	n	38	TYR
7	n	82	VAL
7	n	92	ILE
7	n	99	TYR
7	n	108	THR
1	o	11	ILE
1	o	54	VAL
1	o	68	VAL
1	o	109	ILE

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Mol	Chain	Res	Type
1	o	121	ILE
1	o	130	HIS
1	o	140	LYS
1	o	145	VAL
1	o	147	ILE
1	o	159	GLU
1	o	167	ILE
1	o	172	ILE
1	o	257	ILE
1	o	274	VAL
1	o	291	ARG
1	o	293	ARG
1	o	298	VAL
1	o	351	THR
1	o	355	GLN
1	o	410	ASN
1	o	413	ASP
1	o	434	ILE
1	o	437	ARG
1	o	464	MET
1	o	469	ILE
2	p	20	THR
2	p	33	LEU
2	p	35	VAL
2	p	44	GLN
2	p	47	LEU
2	p	53	LEU
2	p	58	THR
2	p	62	LYS
2	p	77	LEU
2	p	88	PHE
2	p	91	THR
2	p	93	ARG
2	p	109	TRP
2	p	112	VAL
2	p	118	ASN
2	p	123	SER
2	p	136	ILE
2	p	139	ARG
2	p	165	TYR
2	p	180	ASN
2	p	200	ILE

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Mol	Chain	Res	Type
2	p	208	GLU
2	p	214	VAL
2	p	217	THR
2	p	237	ILE
2	p	238	LEU
2	p	239	THR
4	q	5	VAL
4	q	17	LEU
4	q	22	LEU
4	q	35	ARG
4	q	68	VAL
4	q	100	MET
4	q	103	THR
4	q	111	TYR
4	q	120	ILE
4	q	143	VAL
4	q	150	THR
4	q	151	VAL
5	r	4	THR
5	r	25	GLU
5	r	66	GLN
5	r	77	LEU
5	r	80	VAL
5	r	82	ILE
5	r	96	THR
5	r	101	SER
5	r	115	VAL
5	r	125	THR
6	s	3	THR
6	s	8	THR
6	s	18	ARG
6	s	23	ILE
6	s	26	ILE
6	s	44	ASP
6	s	48	GLU
6	s	65	ILE
6	s	68	ASP
7	t	11	ASP
7	t	15	ILE
7	t	26	VAL
7	t	77	MET
7	t	92	ILE

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Mol	Chain	Res	Type
7	t	99	TYR
7	t	104	THR
7	t	108	THR
1	u	29	PHE
1	u	33	VAL
1	u	65	ILE
1	u	85	LEU
1	u	128	VAL
1	u	130	HIS
1	u	147	ILE
1	u	159	GLU
1	u	165	ASP
1	u	169	THR
1	u	170	THR
1	u	191	LEU
1	u	218	ASP
1	u	226	GLU
1	u	234	GLN
1	u	257	ILE
1	u	271	ILE
1	u	288	LEU
1	u	290	GLU
1	u	293	ARG
1	u	298	VAL
1	u	325	ASN
1	u	399	ILE
1	u	410	ASN
1	u	428	LYS
1	u	434	ILE
1	u	435	TYR
1	u	464	MET
1	u	468	GLU
1	u	469	ILE
2	v	33	LEU
2	v	54	ARG
2	v	56	LEU
2	v	66	ILE
2	v	77	LEU
2	v	78	VAL
2	v	88	PHE
2	v	91	THR
2	v	93	ARG

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Mol	Chain	Res	Type
2	v	112	VAL
2	v	123	SER
2	v	136	ILE
2	v	139	ARG
2	v	145	GLU
2	v	152	LYS
2	v	163	GLU
2	v	170	VAL
2	v	180	ASN
2	v	208	GLU
2	v	214	VAL
2	v	217	THR
2	v	239	THR
4	w	35	ARG
4	w	39	MET
4	w	53	ARG
4	w	55	LEU
4	w	78	GLU
4	w	79	GLN
4	w	96	HIS
4	w	109	ASN
4	w	120	ILE
4	w	122	ASN
4	w	143	VAL
4	w	150	THR
5	x	8	ARG
5	x	11	VAL
5	x	25	GLU
5	x	47	GLU
5	x	80	VAL
5	x	82	ILE
5	x	105	LEU
6	y	3	THR
6	y	15	ARG
6	y	17	TYR
6	y	23	ILE
6	y	26	ILE
6	y	37	ARG
6	y	53	ILE
6	y	65	ILE
6	y	113	LEU
7	z	1	MET

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Mol	Chain	Res	Type
7	z	26	VAL
7	z	29	VAL
7	z	35	ILE
7	z	38	TYR
7	z	82	VAL
7	z	92	ILE
7	z	108	THR
9	J	2	LYS
9	J	5	ASP
9	J	7	VAL
9	J	11	THR
9	J	14	ASN
9	J	21	VAL
9	J	24	THR
9	J	27	HIS
9	J	70	ILE
9	J	73	THR
9	J	97	VAL
9	J	108	ASP
9	J	113	LEU
9	J	123	THR
9	J	141	ILE
9	J	176	LYS
9	J	180	ASN
9	J	182	VAL
9	J	183	CYS
9	J	188	ILE
9	J	207	THR
9	J	208	LYS
9	J	210	VAL
9	J	211	GLN
9	J	220	THR
9	J	227	PHE
9	J	236	GLN
9	J	241	ARG
9	J	262	VAL
9	J	267	ASP
9	J	292	GLU
9	J	298	LEU
9	J	300	GLN
9	T	2	LYS
9	T	5	ASP

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Mol	Chain	Res	Type
9	T	7	VAL
9	T	14	ASN
9	T	24	THR
9	T	27	HIS
9	T	38	GLN
9	T	70	ILE
9	T	73	THR
9	T	77	THR
9	T	85	LYS
9	T	86	GLU
9	T	89	THR
9	T	97	VAL
9	T	113	LEU
9	T	141	ILE
9	T	157	THR
9	T	170	GLN
9	T	172	ARG
9	T	180	ASN
9	T	188	ILE
9	T	206	THR
9	T	207	THR
9	T	210	VAL
9	T	211	GLN
9	T	220	THR
9	T	227	PHE
9	T	236	GLN
9	T	241	ARG
9	T	252	LEU
9	T	262	VAL
9	T	292	GLU
9	T	298	LEU
9	T	300	GLN
9	d	5	ASP
9	d	7	VAL
9	d	11	THR
9	d	14	ASN
9	d	21	VAL
9	d	24	THR
9	d	27	HIS
9	d	38	GLN
9	d	69	ASN
9	d	70	ILE

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Mol	Chain	Res	Type
9	d	73	THR
9	d	77	THR
9	d	97	VAL
9	d	113	LEU
9	d	123	THR
9	d	141	ILE
9	d	157	THR
9	d	182	VAL
9	d	188	ILE
9	d	207	THR
9	d	208	LYS
9	d	210	VAL
9	d	211	GLN
9	d	220	THR
9	d	227	PHE
9	d	241	ARG
9	d	262	VAL
9	d	267	ASP
9	d	298	LEU
10	5	695	GLN
10	8	773	ILE
10	9	753	MET
10	9	756	GLU
10	9	758	GLN
10	9	768	VAL
10	9	773	ILE
10	9	783	SER
10	AA	753	MET
10	AA	758	GLN
10	AA	768	VAL
10	AA	773	ILE
10	AA	783	SER
11	AE	5	MET
11	AE	20	LYS
11	AE	35	GLU
11	AE	36	LEU
11	AE	40	GLN
11	AE	57	ASN
11	AE	61	ILE
11	AE	69	GLU
11	AE	71	GLN
11	AE	111	PHE

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Mol	Chain	Res	Type
11	AE	113	ASP
11	AE	140	VAL
11	AE	177	GLN
11	AE	201	VAL
11	AE	218	LYS
11	AE	227	GLN
11	AE	232	LYS
11	AE	262	PHE
11	AE	282	LEU
11	AE	292	GLU
11	AE	295	PHE
11	AE	308	LYS
11	AE	331	LYS
11	AE	338	LEU
11	AE	341	THR
11	AE	380	ASN
11	AE	410	ILE
11	AE	433	ASP
11	AE	436	ARG
11	AE	447	ILE
11	AE	454	VAL
11	AE	475	THR
11	AE	486	TRP
11	AF	13	ILE
11	AF	35	GLU
11	AF	36	LEU
11	AF	46	GLU
11	AF	57	ASN
11	AF	69	GLU
11	AF	74	LEU
11	AF	89	ARG
11	AF	95	ILE
11	AF	98	ASP
11	AF	126	ARG
11	AF	134	LEU
11	AF	144	ARG
11	AF	162	LYS
11	AF	163	HIS
11	AF	169	VAL
11	AF	204	VAL
11	AF	218	LYS
11	AF	233	LYS

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Mol	Chain	Res	Type
11	AF	254	THR
11	AF	261	THR
11	AF	282	LEU
11	AF	297	ARG
11	AF	317	LEU
11	AF	318	THR
11	AF	341	THR
11	AF	374	VAL
11	AF	399	THR
11	AF	406	ASN
11	AF	410	ILE
11	AF	433	ASP
11	AF	435	THR
11	AF	436	ARG
11	AF	454	VAL
11	AF	459	ASN
11	AF	477	PHE
11	AF	482	ASN
11	AF	485	ASN
11	AG	17	ASN
11	AG	22	ASP
11	AG	30	LEU
11	AG	89	ARG
11	AG	113	ASP
11	AG	131	TYR
11	AG	134	LEU
11	AG	154	GLU
11	AG	162	LYS
11	AG	177	GLN
11	AG	190	LEU
11	AG	233	LYS
11	AG	261	THR
11	AG	282	LEU
11	AG	293	THR
11	AG	300	GLN
11	AG	328	VAL
11	AG	329	MET
11	AG	331	LYS
11	AG	335	LEU
11	AG	338	LEU
11	AG	370	ASP
11	AG	391	VAL

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Mol	Chain	Res	Type
11	AG	394	LEU
11	AG	407	GLN
11	AG	410	ILE
11	AG	416	ARG
11	AG	424	GLN
11	AG	434	ASP
11	AG	436	ARG
11	AG	454	VAL
11	AG	469	THR
11	AG	488	TYR
11	AG	499	LEU
11	AB	20	LYS
11	AB	35	GLU
11	AB	36	LEU
11	AB	61	ILE
11	AB	90	THR
11	AB	98	ASP
11	AB	108	ARG
11	AB	134	LEU
11	AB	161	MET
11	AB	177	GLN
11	AB	227	GLN
11	AB	294	TYR
11	AB	295	PHE
11	AB	308	LYS
11	AB	320	MET
11	AB	331	LYS
11	AB	338	LEU
11	AB	360	ASP
11	AB	391	VAL
11	AB	410	ILE
11	AB	431	LEU
11	AB	436	ARG
11	AB	439	ILE
11	AB	454	VAL
11	AB	455	MET
11	AB	462	ILE
11	AB	469	THR
11	AB	481	CYS
11	AB	491	ASN
11	AB	499	LEU
11	AC	35	GLU

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Mol	Chain	Res	Type
11	AC	36	LEU
11	AC	57	ASN
11	AC	74	LEU
11	AC	77	THR
11	AC	83	ILE
11	AC	98	ASP
11	AC	134	LEU
11	AC	144	ARG
11	AC	162	LYS
11	AC	163	HIS
11	AC	195	THR
11	AC	204	VAL
11	AC	218	LYS
11	AC	233	LYS
11	AC	261	THR
11	AC	302	LEU
11	AC	304	ASP
11	AC	315	LEU
11	AC	330	MET
11	AC	407	GLN
11	AC	410	ILE
11	AC	436	ARG
11	AC	441	LEU
11	AC	457	THR
11	AC	469	THR
11	AC	486	TRP
11	AC	491	ASN
11	AC	496	THR
11	AD	3	ASN
11	AD	4	ILE
11	AD	19	GLN
11	AD	22	ASP
11	AD	30	LEU
11	AD	33	VAL
11	AD	93	ASP
11	AD	133	THR
11	AD	162	LYS
11	AD	177	GLN
11	AD	211	GLU
11	AD	233	LYS
11	AD	261	THR
11	AD	268	ASN

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Mol	Chain	Res	Type
11	AD	282	LEU
11	AD	315	LEU
11	AD	328	VAL
11	AD	331	LYS
11	AD	333	ASP
11	AD	338	LEU
11	AD	388	THR
11	AD	394	LEU
11	AD	399	THR
11	AD	410	ILE
11	AD	424	GLN
11	AD	436	ARG
11	AD	454	VAL
11	AD	462	ILE
11	AD	485	ASN
11	AD	486	TRP
11	AD	498	THR
11	AH	5	MET
11	AH	20	LYS
11	AH	35	GLU
11	AH	40	GLN
11	AH	61	ILE
11	AH	69	GLU
11	AH	98	ASP
11	AH	111	PHE
11	AH	113	ASP
11	AH	140	VAL
11	AH	177	GLN
11	AH	218	LYS
11	AH	227	GLN
11	AH	232	LYS
11	AH	234	ASP
11	AH	262	PHE
11	AH	282	LEU
11	AH	292	GLU
11	AH	295	PHE
11	AH	298	SER
11	AH	324	ASP
11	AH	331	LYS
11	AH	338	LEU
11	AH	366	ASP
11	AH	380	ASN

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Mol	Chain	Res	Type
11	AH	410	ILE
11	AH	422	LEU
11	AH	433	ASP
11	AH	436	ARG
11	AH	447	ILE
11	AH	454	VAL
11	AH	475	THR
11	AH	486	TRP
11	AI	13	ILE
11	AI	35	GLU
11	AI	46	GLU
11	AI	57	ASN
11	AI	69	GLU
11	AI	71	GLN
11	AI	74	LEU
11	AI	83	ILE
11	AI	89	ARG
11	AI	95	ILE
11	AI	98	ASP
11	AI	134	LEU
11	AI	144	ARG
11	AI	163	HIS
11	AI	170	PHE
11	AI	204	VAL
11	AI	218	LYS
11	AI	233	LYS
11	AI	254	THR
11	AI	261	THR
11	AI	282	LEU
11	AI	297	ARG
11	AI	302	LEU
11	AI	317	LEU
11	AI	318	THR
11	AI	341	THR
11	AI	348	LEU
11	AI	374	VAL
11	AI	399	THR
11	AI	406	ASN
11	AI	410	ILE
11	AI	435	THR
11	AI	436	ARG
11	AI	459	ASN

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Mol	Chain	Res	Type
11	AI	477	PHE
11	AI	485	ASN
11	AJ	17	ASN
11	AJ	22	ASP
11	AJ	30	LEU
11	AJ	89	ARG
11	AJ	113	ASP
11	AJ	131	TYR
11	AJ	134	LEU
11	AJ	158	ARG
11	AJ	162	LYS
11	AJ	170	PHE
11	AJ	177	GLN
11	AJ	190	LEU
11	AJ	223	LEU
11	AJ	231	LYS
11	AJ	233	LYS
11	AJ	261	THR
11	AJ	282	LEU
11	AJ	323	THR
11	AJ	331	LYS
11	AJ	335	LEU
11	AJ	338	LEU
11	AJ	360	ASP
11	AJ	370	ASP
11	AJ	391	VAL
11	AJ	394	LEU
11	AJ	407	GLN
11	AJ	410	ILE
11	AJ	416	ARG
11	AJ	434	ASP
11	AJ	436	ARG
11	AJ	449	ASN
11	AJ	454	VAL
11	AJ	469	THR
11	AJ	488	TYR
11	AJ	499	LEU
11	AK	20	LYS
11	AK	21	VAL
11	AK	35	GLU
11	AK	61	ILE
11	AK	90	THR

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Mol	Chain	Res	Type
11	AK	98	ASP
11	AK	108	ARG
11	AK	134	LEU
11	AK	140	VAL
11	AK	145	GLN
11	AK	162	LYS
11	AK	169	VAL
11	AK	227	GLN
11	AK	234	ASP
11	AK	294	TYR
11	AK	295	PHE
11	AK	301	ASN
11	AK	308	LYS
11	AK	331	LYS
11	AK	338	LEU
11	AK	345	ARG
11	AK	360	ASP
11	AK	391	VAL
11	AK	406	ASN
11	AK	408	SER
11	AK	424	GLN
11	AK	436	ARG
11	AK	454	VAL
11	AK	455	MET
11	AK	462	ILE
11	AK	479	VAL
11	AK	491	ASN
11	AL	19	GLN
11	AL	35	GLU
11	AL	57	ASN
11	AL	74	LEU
11	AL	83	ILE
11	AL	98	ASP
11	AL	134	LEU
11	AL	142	ILE
11	AL	144	ARG
11	AL	163	HIS
11	AL	195	THR
11	AL	221	SER
11	AL	233	LYS
11	AL	261	THR
11	AL	293	THR

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Mol	Chain	Res	Type
11	AL	302	LEU
11	AL	304	ASP
11	AL	315	LEU
11	AL	320	MET
11	AL	330	MET
11	AL	341	THR
11	AL	410	ILE
11	AL	424	GLN
11	AL	436	ARG
11	AL	457	THR
11	AL	486	TRP
11	AL	496	THR
11	AM	3	ASN
11	AM	4	ILE
11	AM	17	ASN
11	AM	19	GLN
11	AM	22	ASP
11	AM	30	LEU
11	AM	33	VAL
11	AM	93	ASP
11	AM	162	LYS
11	AM	177	GLN
11	AM	211	GLU
11	AM	233	LYS
11	AM	261	THR
11	AM	304	ASP
11	AM	315	LEU
11	AM	323	THR
11	AM	328	VAL
11	AM	329	MET
11	AM	331	LYS
11	AM	333	ASP
11	AM	335	LEU
11	AM	338	LEU
11	AM	394	LEU
11	AM	399	THR
11	AM	410	ILE
11	AM	412	ARG
11	AM	424	GLN
11	AM	436	ARG
11	AM	440	GLN
11	AM	454	VAL

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Mol	Chain	Res	Type
11	AM	462	ILE
11	AM	478	ARG
11	AM	485	ASN
11	AM	486	TRP
11	AM	496	THR
11	AM	498	THR
11	AN	5	MET
11	AN	20	LYS
11	AN	36	LEU
11	AN	40	GLN
11	AN	61	ILE
11	AN	98	ASP
11	AN	113	ASP
11	AN	140	VAL
11	AN	177	GLN
11	AN	202	MET
11	AN	227	GLN
11	AN	232	LYS
11	AN	259	SER
11	AN	262	PHE
11	AN	331	LYS
11	AN	338	LEU
11	AN	366	ASP
11	AN	380	ASN
11	AN	410	ILE
11	AN	427	THR
11	AN	433	ASP
11	AN	436	ARG
11	AN	447	ILE
11	AN	454	VAL
11	AN	475	THR
11	AN	486	TRP
11	AO	3	ASN
11	AO	13	ILE
11	AO	35	GLU
11	AO	36	LEU
11	AO	46	GLU
11	AO	57	ASN
11	AO	69	GLU
11	AO	71	GLN
11	AO	74	LEU
11	AO	83	ILE

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Mol	Chain	Res	Type
11	AO	89	ARG
11	AO	95	ILE
11	AO	98	ASP
11	AO	134	LEU
11	AO	137	ILE
11	AO	162	LYS
11	AO	163	HIS
11	AO	170	PHE
11	AO	204	VAL
11	AO	218	LYS
11	AO	233	LYS
11	AO	254	THR
11	AO	261	THR
11	AO	297	ARG
11	AO	302	LEU
11	AO	317	LEU
11	AO	318	THR
11	AO	341	THR
11	AO	348	LEU
11	AO	374	VAL
11	AO	399	THR
11	AO	406	ASN
11	AO	407	GLN
11	AO	410	ILE
11	AO	433	ASP
11	AO	435	THR
11	AO	436	ARG
11	AO	454	VAL
11	AO	477	PHE
11	AO	485	ASN
11	AP	17	ASN
11	AP	30	LEU
11	AP	56	VAL
11	AP	89	ARG
11	AP	113	ASP
11	AP	131	TYR
11	AP	134	LEU
11	AP	162	LYS
11	AP	177	GLN
11	AP	190	LEU
11	AP	223	LEU
11	AP	233	LYS

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Mol	Chain	Res	Type
11	AP	261	THR
11	AP	269	LEU
11	AP	282	LEU
11	AP	296	LEU
11	AP	300	GLN
11	AP	329	MET
11	AP	331	LYS
11	AP	338	LEU
11	AP	370	ASP
11	AP	391	VAL
11	AP	394	LEU
11	AP	399	THR
11	AP	410	ILE
11	AP	416	ARG
11	AP	424	GLN
11	AP	434	ASP
11	AP	436	ARG
11	AP	454	VAL
11	AP	469	THR
11	AP	488	TYR
11	AP	499	LEU
11	AQ	20	LYS
11	AQ	35	GLU
11	AQ	36	LEU
11	AQ	61	ILE
11	AQ	71	GLN
11	AQ	90	THR
11	AQ	108	ARG
11	AQ	134	LEU
11	AQ	140	VAL
11	AQ	144	ARG
11	AQ	161	MET
11	AQ	162	LYS
11	AQ	169	VAL
11	AQ	177	GLN
11	AQ	196	GLU
11	AQ	227	GLN
11	AQ	294	TYR
11	AQ	295	PHE
11	AQ	308	LYS
11	AQ	315	LEU
11	AQ	322	THR

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Mol	Chain	Res	Type
11	AQ	329	MET
11	AQ	335	LEU
11	AQ	338	LEU
11	AQ	345	ARG
11	AQ	380	ASN
11	AQ	410	ILE
11	AQ	436	ARG
11	AQ	438	ASN
11	AQ	447	ILE
11	AQ	493	PHE
11	AQ	499	LEU
11	AR	3	ASN
11	AR	35	GLU
11	AR	57	ASN
11	AR	69	GLU
11	AR	74	LEU
11	AR	77	THR
11	AR	83	ILE
11	AR	98	ASP
11	AR	134	LEU
11	AR	144	ARG
11	AR	163	HIS
11	AR	176	THR
11	AR	177	GLN
11	AR	195	THR
11	AR	201	VAL
11	AR	233	LYS
11	AR	251	LEU
11	AR	261	THR
11	AR	271	ASP
11	AR	293	THR
11	AR	297	ARG
11	AR	333	ASP
11	AR	348	LEU
11	AR	401	MET
11	AR	409	ASP
11	AR	410	ILE
11	AR	436	ARG
11	AR	457	THR
11	AR	460	ASN
11	AR	462	ILE
11	AS	4	ILE

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Mol	Chain	Res	Type
11	AS	22	ASP
11	AS	30	LEU
11	AS	93	ASP
11	AS	162	LYS
11	AS	177	GLN
11	AS	231	LYS
11	AS	233	LYS
11	AS	261	THR
11	AS	275	LYS
11	AS	282	LEU
11	AS	297	ARG
11	AS	315	LEU
11	AS	328	VAL
11	AS	331	LYS
11	AS	335	LEU
11	AS	340	ASN
11	AS	341	THR
11	AS	394	LEU
11	AS	399	THR
11	AS	409	ASP
11	AS	410	ILE
11	AS	427	THR
11	AS	436	ARG
11	AS	439	ILE
11	AS	454	VAL
11	AS	462	ILE
11	AS	485	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (280) such sidechains are listed below:

Mol	Chain	Res	Type
1	0	73	ASN
1	0	329	ASN
1	0	388	GLN
1	0	410	ASN
1	0	466	ASN
2	1	4	ASN
2	1	22	GLN
2	1	44	GLN
2	1	118	ASN
2	1	210	GLN
3	A	43	HIS

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Mol	Chain	Res	Type
3	A	177	ASN
3	B	63	ASN
3	B	185	GLN
3	C	43	HIS
3	C	63	ASN
3	C	86	ASN
3	D	43	HIS
3	D	63	ASN
3	D	75	GLN
3	D	86	ASN
3	D	146	ASN
3	E	24	GLN
3	F	24	GLN
3	F	88	GLN
3	F	185	GLN
3	F	228	ASN
4	G	46	HIS
4	G	47	HIS
4	G	79	GLN
4	G	140	ASN
5	H	53	ASN
5	H	136	ASN
6	I	13	GLN
6	I	51	ASN
6	I	110	ASN
1	L	234	GLN
1	L	294	ASN
1	L	386	ASN
1	M	114	ASN
1	M	199	HIS
1	M	299	GLN
1	M	329	ASN
1	M	360	ASN
1	M	426	ASN
1	M	462	GLN
1	N	234	GLN
2	O	44	GLN
2	O	210	GLN
8	P	93	GLN
8	P	117	ASN
8	P	140	HIS
8	P	227	HIS

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Mol	Chain	Res	Type
4	Q	3	ASN
4	Q	46	HIS
4	Q	47	HIS
5	R	136	ASN
6	S	102	GLN
6	S	110	ASN
7	U	10	HIS
7	U	31	GLN
7	U	95	HIS
1	V	66	GLN
1	V	73	ASN
1	V	339	HIS
1	V	355	GLN
1	V	388	GLN
1	V	410	ASN
1	V	466	ASN
1	W	70	ASN
1	W	84	ASN
1	W	94	HIS
1	W	253	GLN
1	W	329	ASN
1	W	462	GLN
1	X	234	GLN
1	X	299	GLN
2	Y	44	GLN
8	Z	59	GLN
8	Z	108	HIS
8	Z	135	ASN
8	Z	140	HIS
8	Z	245	GLN
4	a	3	ASN
6	c	13	GLN
6	c	51	ASN
6	c	77	ASN
6	c	86	ASN
7	e	10	HIS
7	e	95	HIS
1	f	66	GLN
1	f	374	GLN
1	g	253	GLN
1	g	329	ASN
1	h	234	GLN

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Mol	Chain	Res	Type
1	h	299	GLN
2	i	138	ASN
8	j	93	GLN
8	j	111	ASN
8	j	117	ASN
8	j	205	ASN
8	j	231	HIS
8	j	245	GLN
4	k	3	ASN
4	k	47	HIS
4	k	70	ASN
4	k	96	HIS
4	k	142	GLN
5	l	53	ASN
5	l	71	ASN
5	l	136	ASN
6	m	110	ASN
1	o	66	GLN
1	o	70	ASN
1	o	339	HIS
1	o	388	GLN
1	o	410	ASN
1	o	466	ASN
2	p	22	GLN
2	p	44	GLN
2	p	210	GLN
5	r	136	ASN
6	s	51	ASN
6	s	91	GLN
7	t	10	HIS
7	t	95	HIS
1	u	294	ASN
1	u	388	GLN
2	v	44	GLN
4	w	109	ASN
5	x	53	ASN
5	x	136	ASN
6	y	94	HIS
6	y	110	ASN
7	z	31	GLN
9	J	69	ASN
9	J	96	ASN

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Mol	Chain	Res	Type
9	J	147	GLN
9	J	277	ASN
9	T	33	ASN
9	T	38	GLN
9	T	69	ASN
9	T	96	ASN
9	T	253	ASN
9	d	33	ASN
9	d	38	GLN
9	d	49	ASN
9	d	54	ASN
9	d	96	ASN
9	d	147	GLN
9	d	163	ASN
9	d	191	ASN
9	d	236	GLN
10	4	695	GLN
10	4	705	HIS
10	3	695	GLN
10	AA	784	GLN
11	AE	59	HIS
11	AE	78	GLN
11	AE	168	ASN
11	AE	334	ASN
11	AE	449	ASN
11	AE	451	GLN
11	AF	3	ASN
11	AF	49	GLN
11	AF	101	ASN
11	AF	127	HIS
11	AF	130	ASN
11	AG	55	HIS
11	AG	58	GLN
11	AG	59	HIS
11	AG	163	HIS
11	AG	180	HIS
11	AG	248	ASN
11	AG	310	GLN
11	AG	449	ASN
11	AG	485	ASN
11	AB	57	ASN
11	AB	58	GLN

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Mol	Chain	Res	Type
11	AB	78	GLN
11	AB	163	HIS
11	AB	177	GLN
11	AB	186	GLN
11	AB	310	GLN
11	AB	314	ASN
11	AB	347	ASN
11	AB	367	ASN
11	AB	406	ASN
11	AB	491	ASN
11	AC	40	GLN
11	AC	91	HIS
11	AC	127	HIS
11	AC	132	ASN
11	AC	235	ASN
11	AC	310	GLN
11	AC	459	ASN
11	AD	55	HIS
11	AD	91	HIS
11	AD	146	ASN
11	AD	367	ASN
11	AD	397	ASN
11	AD	407	GLN
11	AD	449	ASN
11	AH	59	HIS
11	AH	165	ASN
11	AH	168	ASN
11	AH	449	ASN
11	AH	451	GLN
11	AH	485	ASN
11	AI	49	GLN
11	AI	57	ASN
11	AI	78	GLN
11	AI	168	ASN
11	AI	177	GLN
11	AI	180	HIS
11	AI	281	ASN
11	AI	340	ASN
11	AJ	43	ASN
11	AJ	58	GLN
11	AJ	59	HIS
11	AJ	132	ASN

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Mol	Chain	Res	Type
11	AJ	300	GLN
11	AJ	310	GLN
11	AJ	334	ASN
11	AJ	485	ASN
11	AK	73	ASN
11	AK	165	ASN
11	AK	168	ASN
11	AK	186	GLN
11	AK	340	ASN
11	AK	375	GLN
11	AK	379	ASN
11	AL	91	HIS
11	AL	123	ASN
11	AL	127	HIS
11	AL	310	GLN
11	AL	419	ASN
11	AM	55	HIS
11	AM	78	GLN
11	AM	91	HIS
11	AM	130	ASN
11	AM	146	ASN
11	AM	367	ASN
11	AM	397	ASN
11	AM	451	GLN
11	AN	43	ASN
11	AN	78	GLN
11	AN	334	ASN
11	AN	449	ASN
11	AN	451	GLN
11	AN	485	ASN
11	AO	3	ASN
11	AO	78	GLN
11	AO	121	GLN
11	AO	177	GLN
11	AO	334	ASN
11	AP	59	HIS
11	AP	91	HIS
11	AP	132	ASN
11	AP	300	GLN
11	AP	310	GLN
11	AP	334	ASN
11	AP	485	ASN

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Mol	Chain	Res	Type
11	AQ	3	ASN
11	AQ	57	ASN
11	AQ	91	HIS
11	AQ	186	GLN
11	AQ	310	GLN
11	AR	40	GLN
11	AR	71	GLN
11	AR	91	HIS
11	AR	127	HIS
11	AR	132	ASN
11	AR	301	ASN
11	AR	314	ASN
11	AR	419	ASN
11	AR	424	GLN
11	AR	485	ASN
11	AS	55	HIS
11	AS	58	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

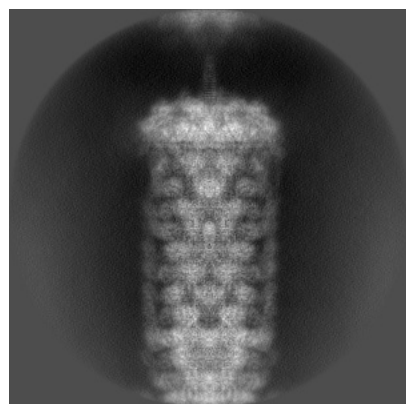
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-74056. These allow visual inspection of the internal detail of the map and identification of artifacts.

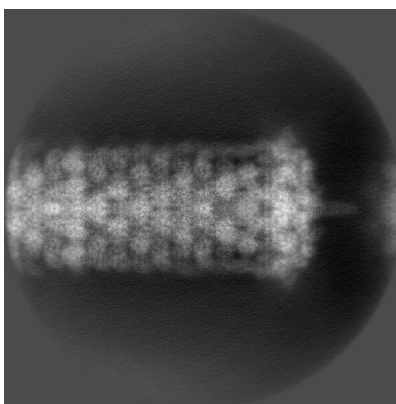
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

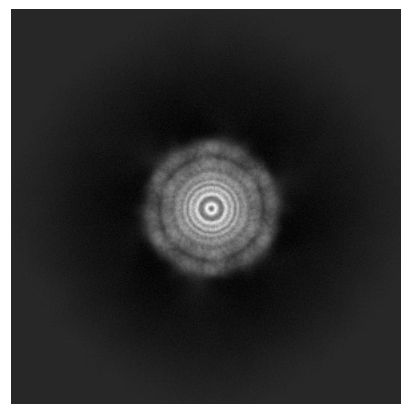
6.1.1 Primary map



X

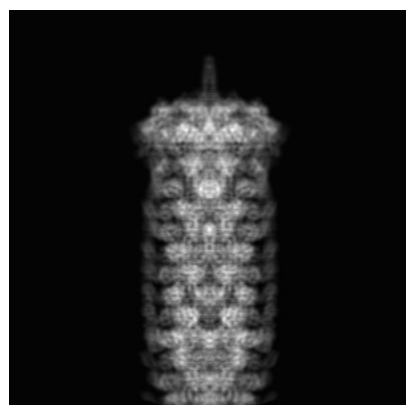


Y

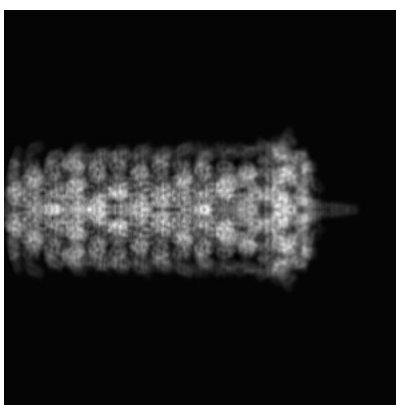


Z

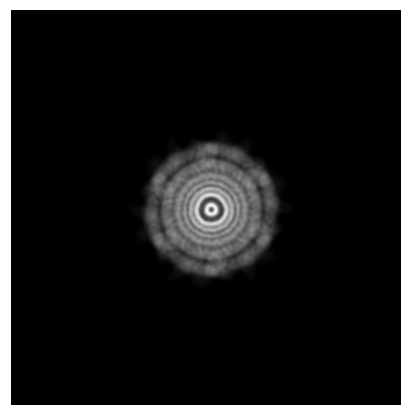
6.1.2 Raw map



X



Y

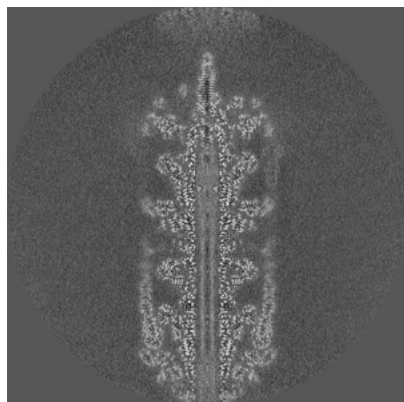


Z

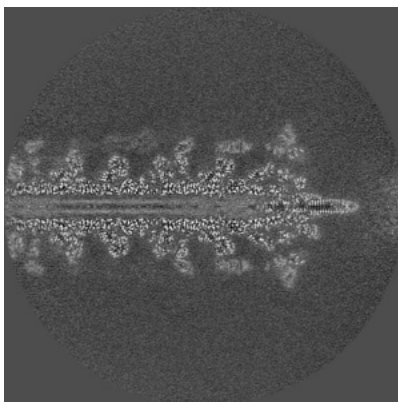
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

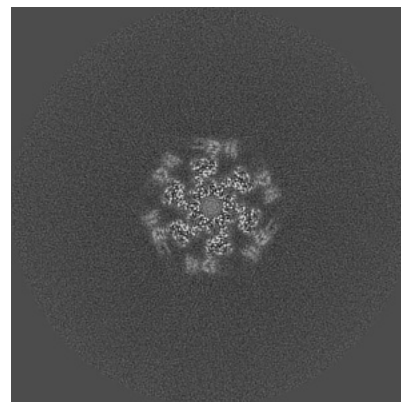
6.2.1 Primary map



X Index: 256

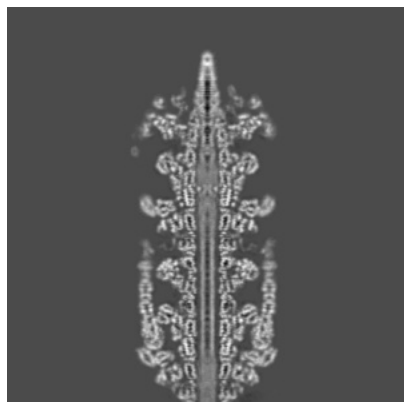


Y Index: 256

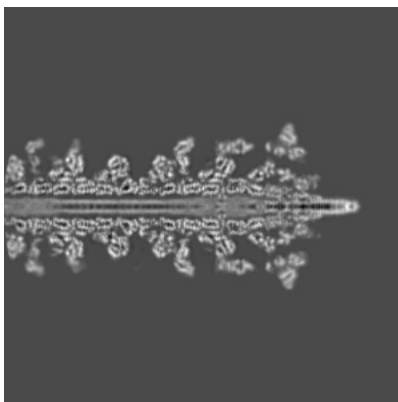


Z Index: 256

6.2.2 Raw map



X Index: 256



Y Index: 256

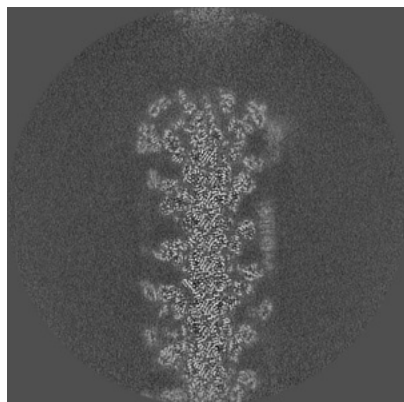


Z Index: 256

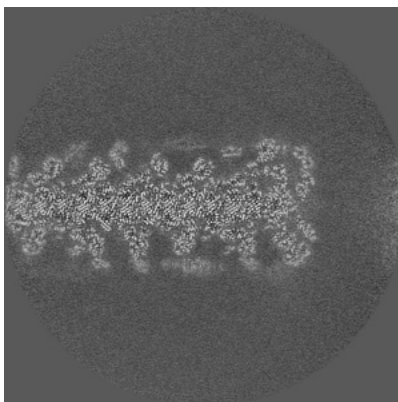
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

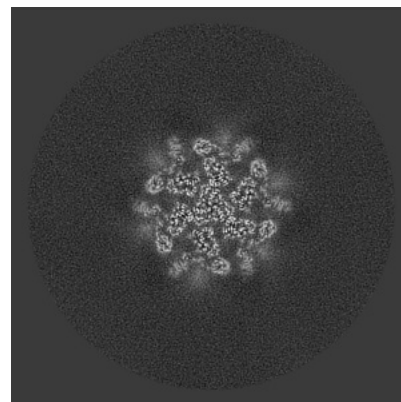
6.3.1 Primary map



X Index: 273

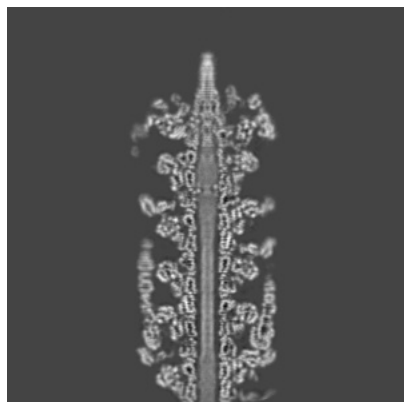


Y Index: 238

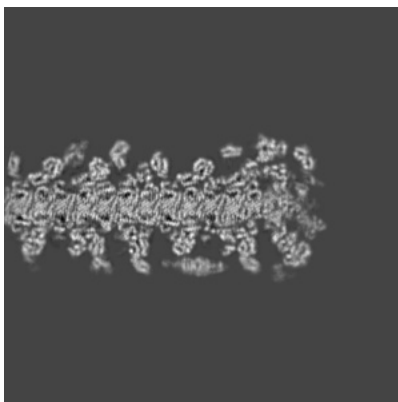


Z Index: 358

6.3.2 Raw map



X Index: 252



Y Index: 238

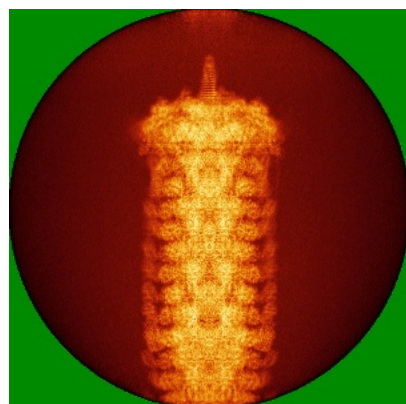


Z Index: 358

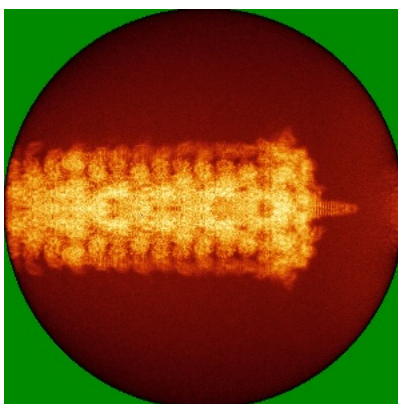
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) [i](#)

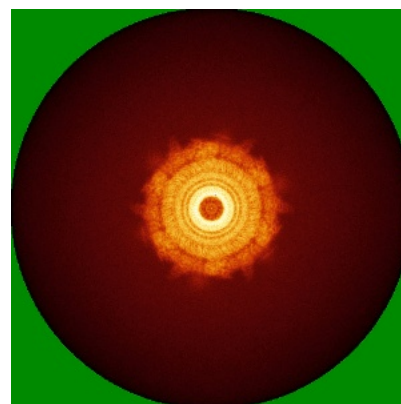
6.4.1 Primary map



X

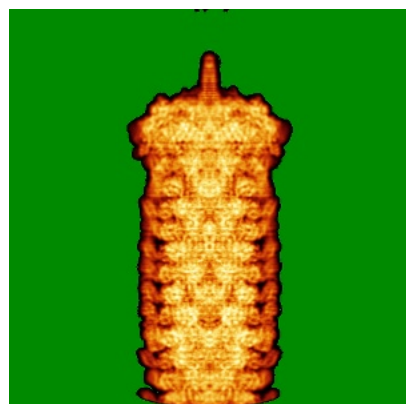


Y

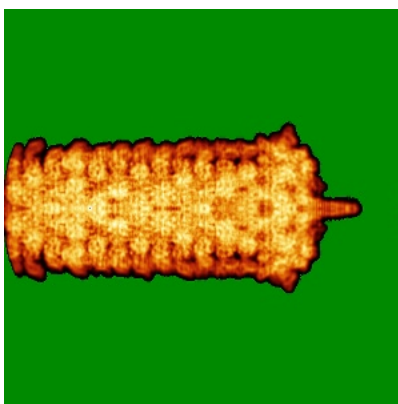


Z

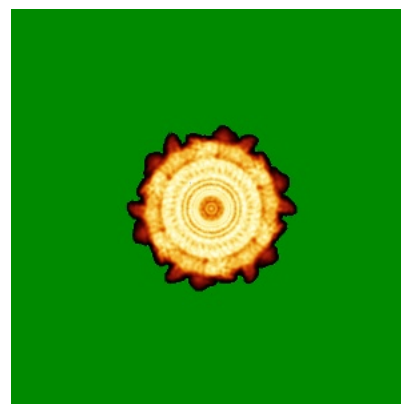
6.4.2 Raw map



X



Y

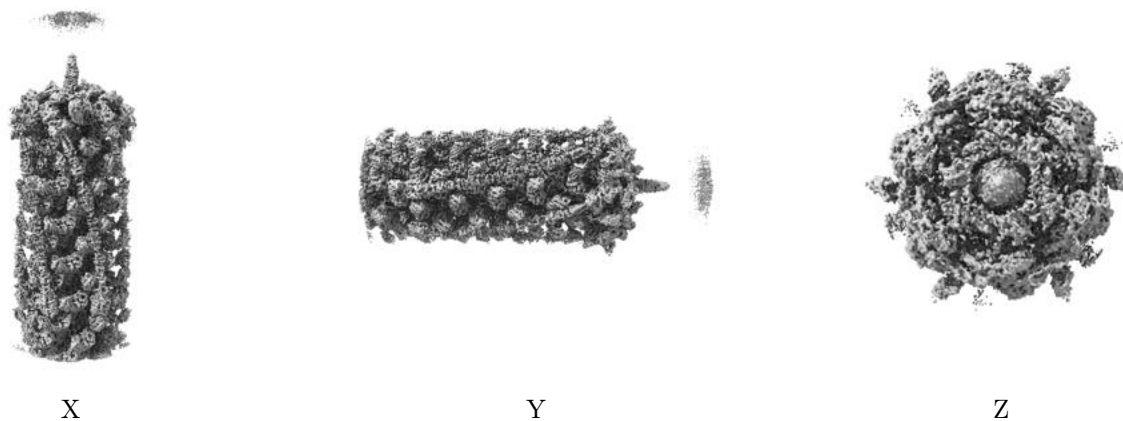


Z

The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

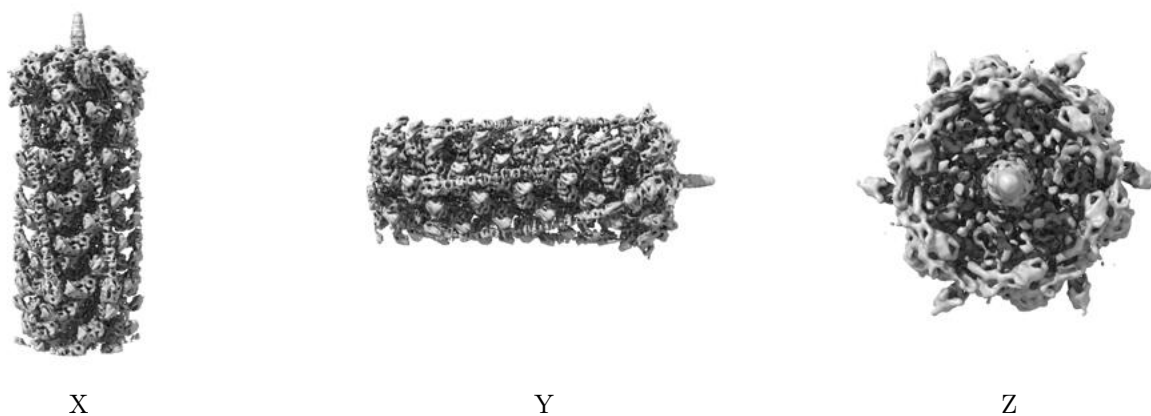
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.0202. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

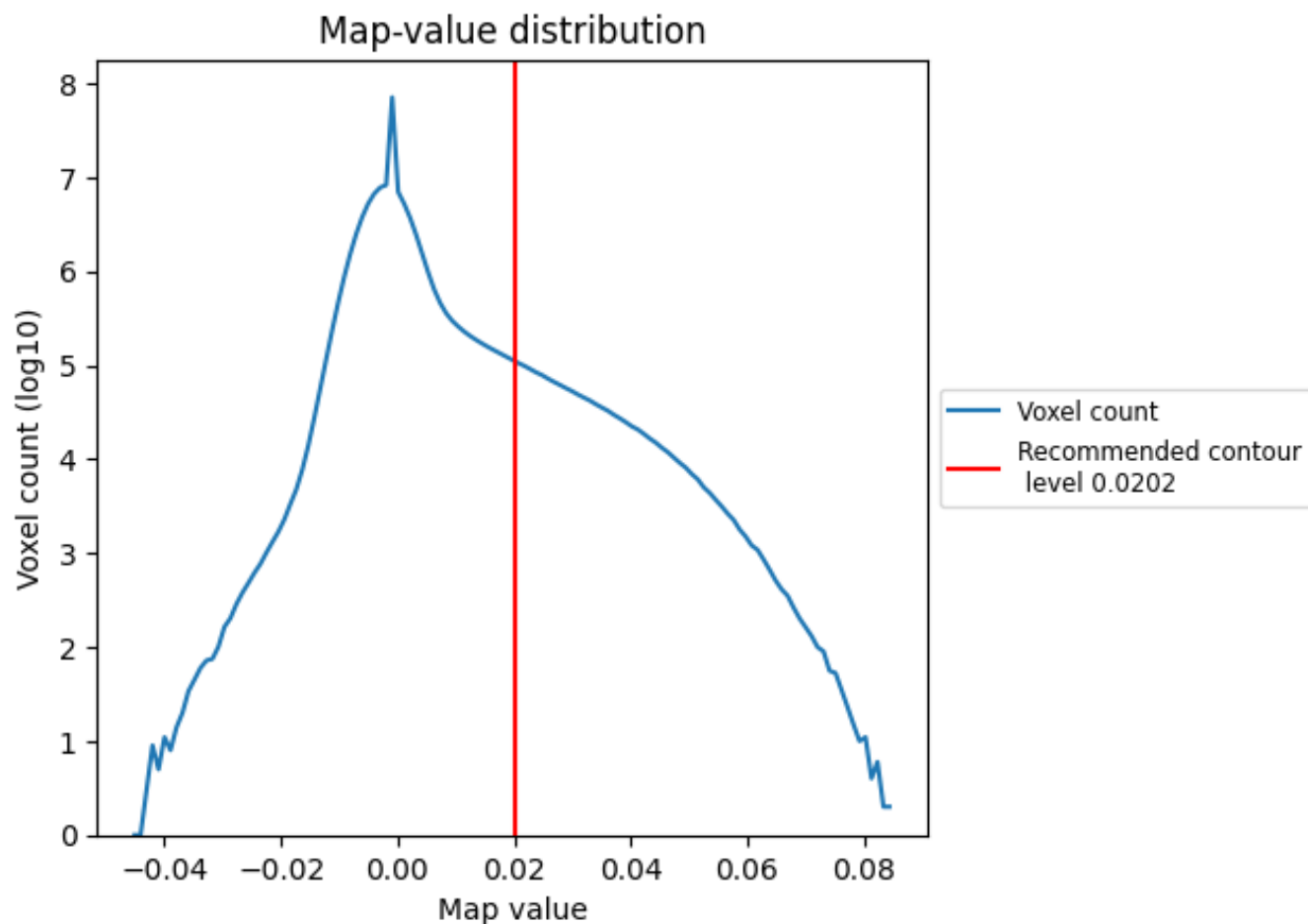
6.6 Mask visualisation [i](#)

This section was not generated. No masks/segmentation were deposited.

7 Map analysis [i](#)

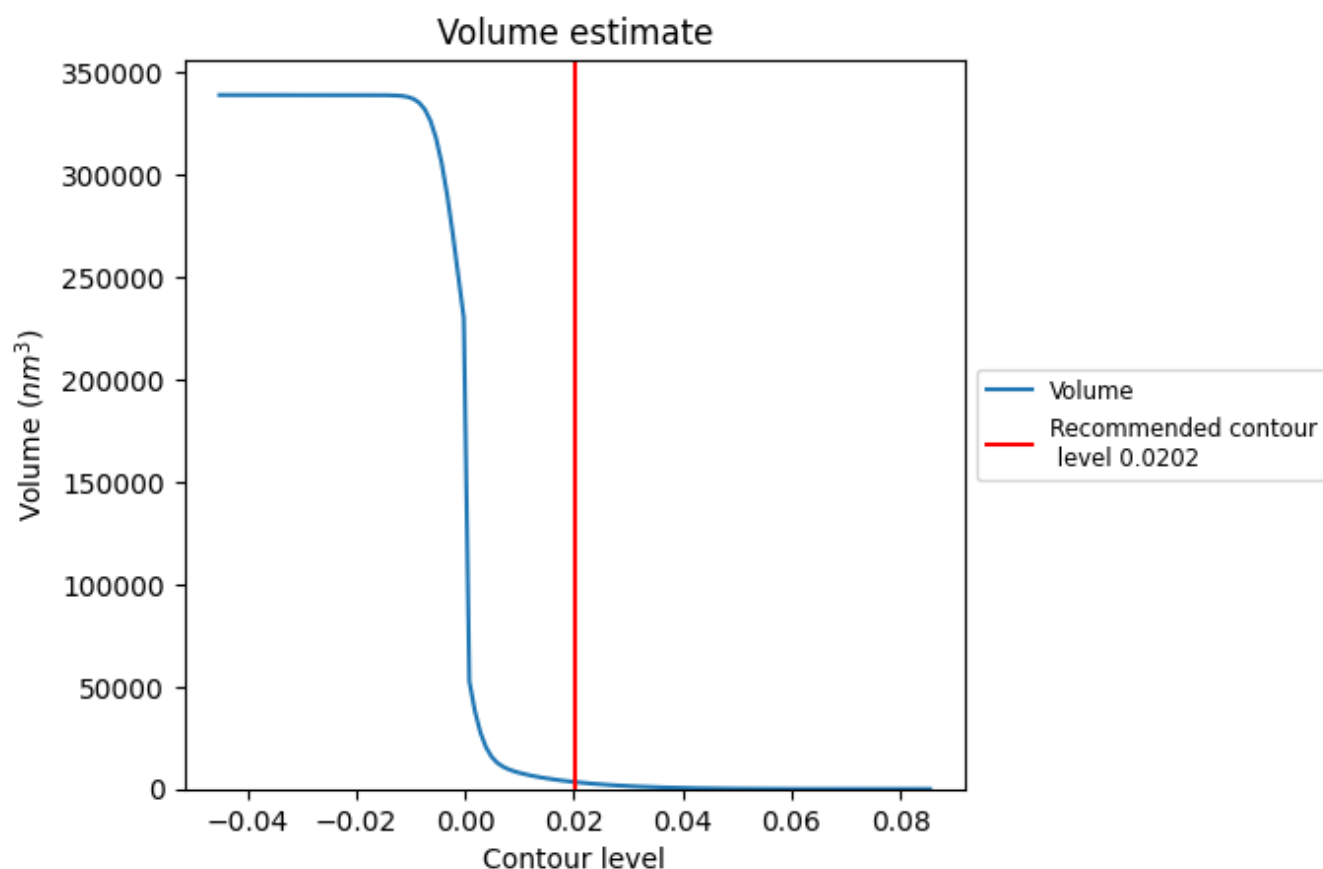
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

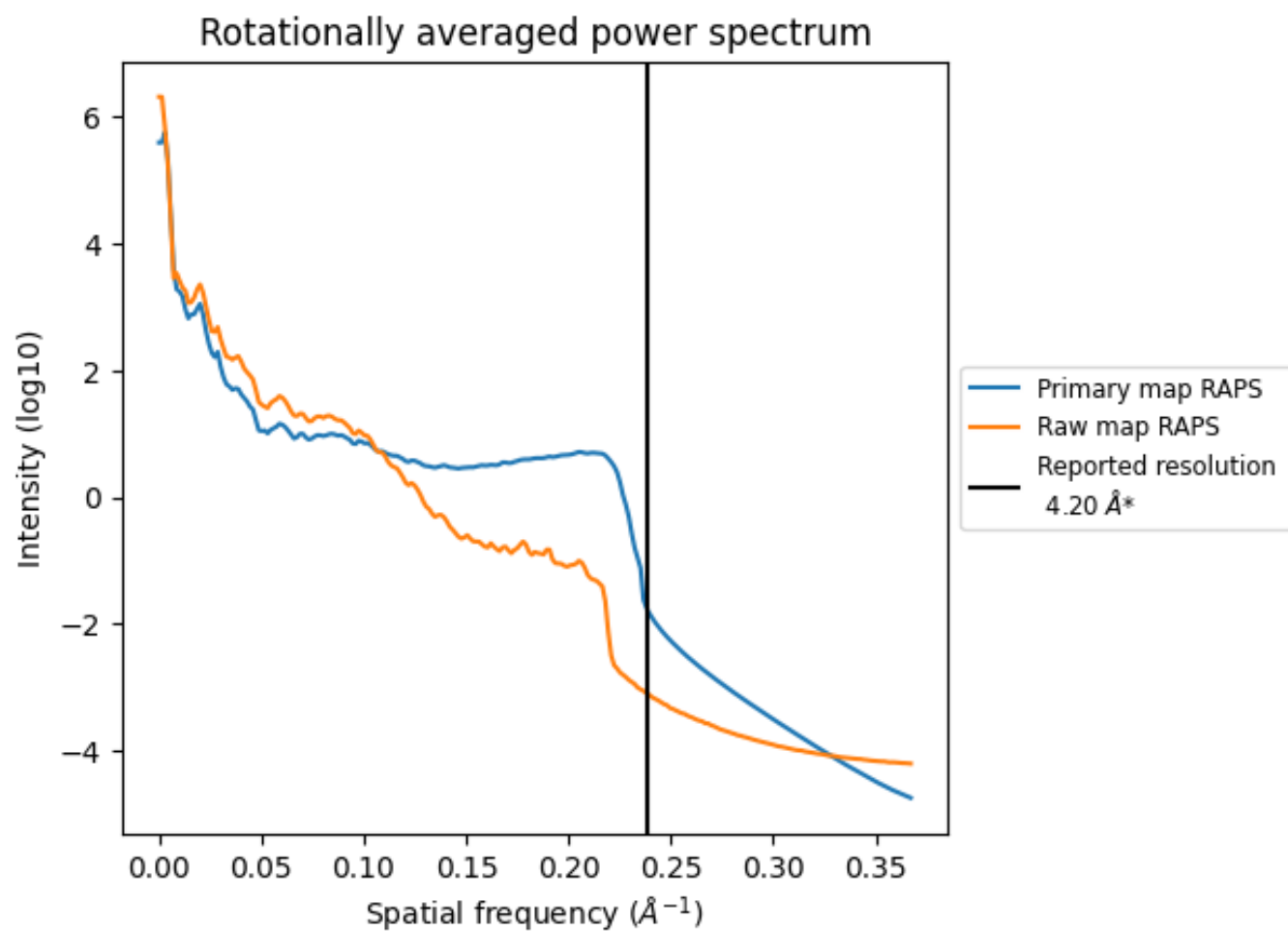
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 3370 nm^3 ; this corresponds to an approximate mass of 3044 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum ⓘ

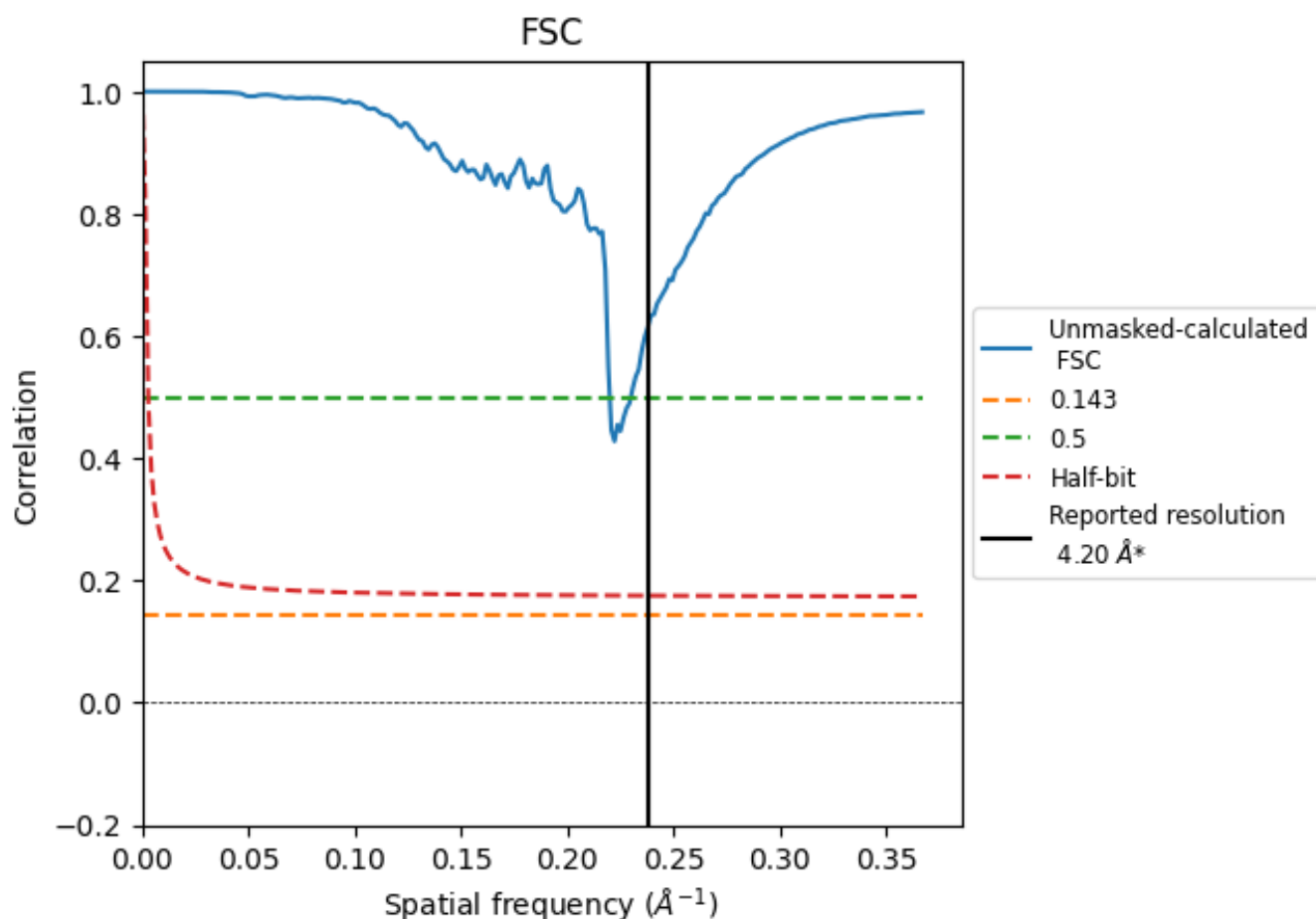


*Reported resolution corresponds to spatial frequency of 0.238 Å⁻¹

8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.238 Å⁻¹

8.2 Resolution estimates [i](#)

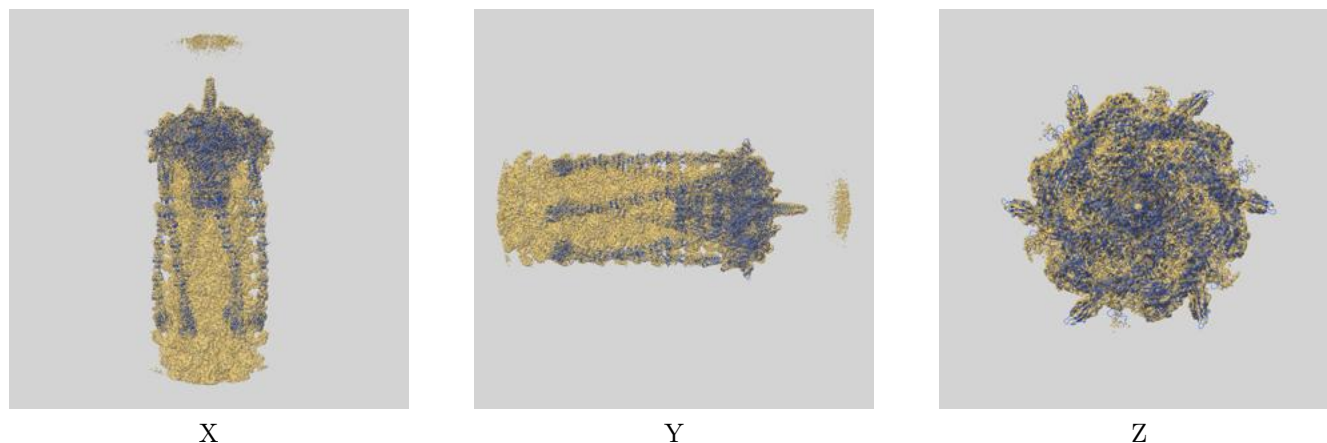
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.20	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	-	4.54	-

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

9 Map-model fit [i](#)

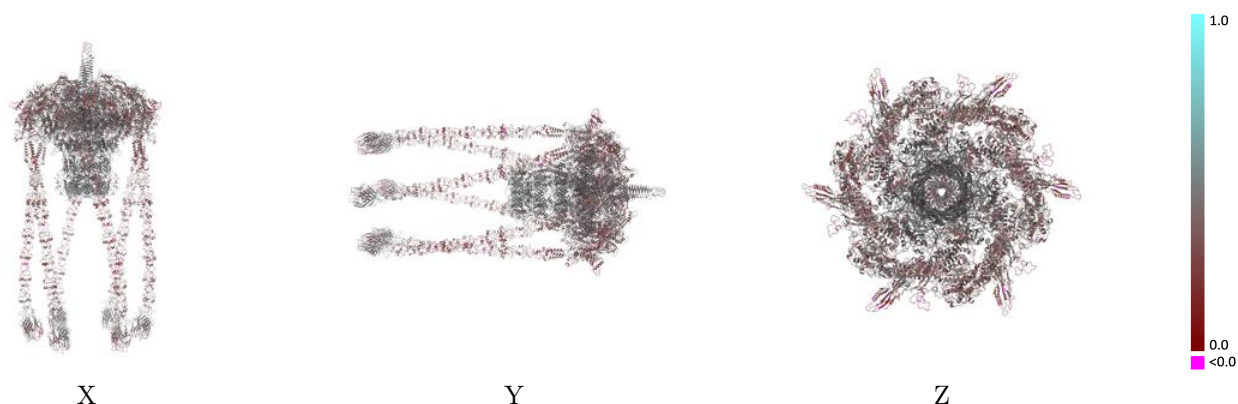
This section contains information regarding the fit between EMDB map EMD-74056 and PDB model 9ZD7. Per-residue inclusion information can be found in section [3](#) on page [12](#).

9.1 Map-model overlay [i](#)



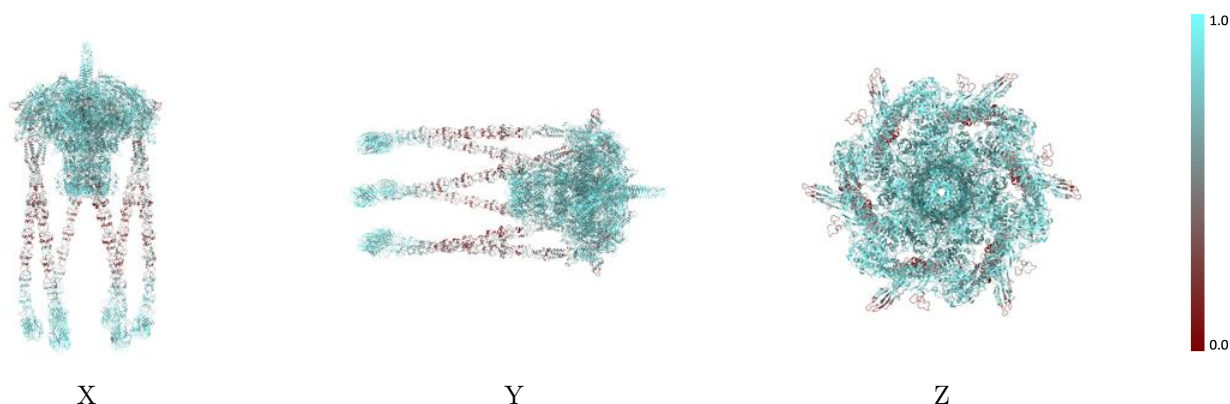
The images above show the 3D surface view of the map at the recommended contour level 0.0202 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

9.2 Q-score mapped to coordinate model [i](#)



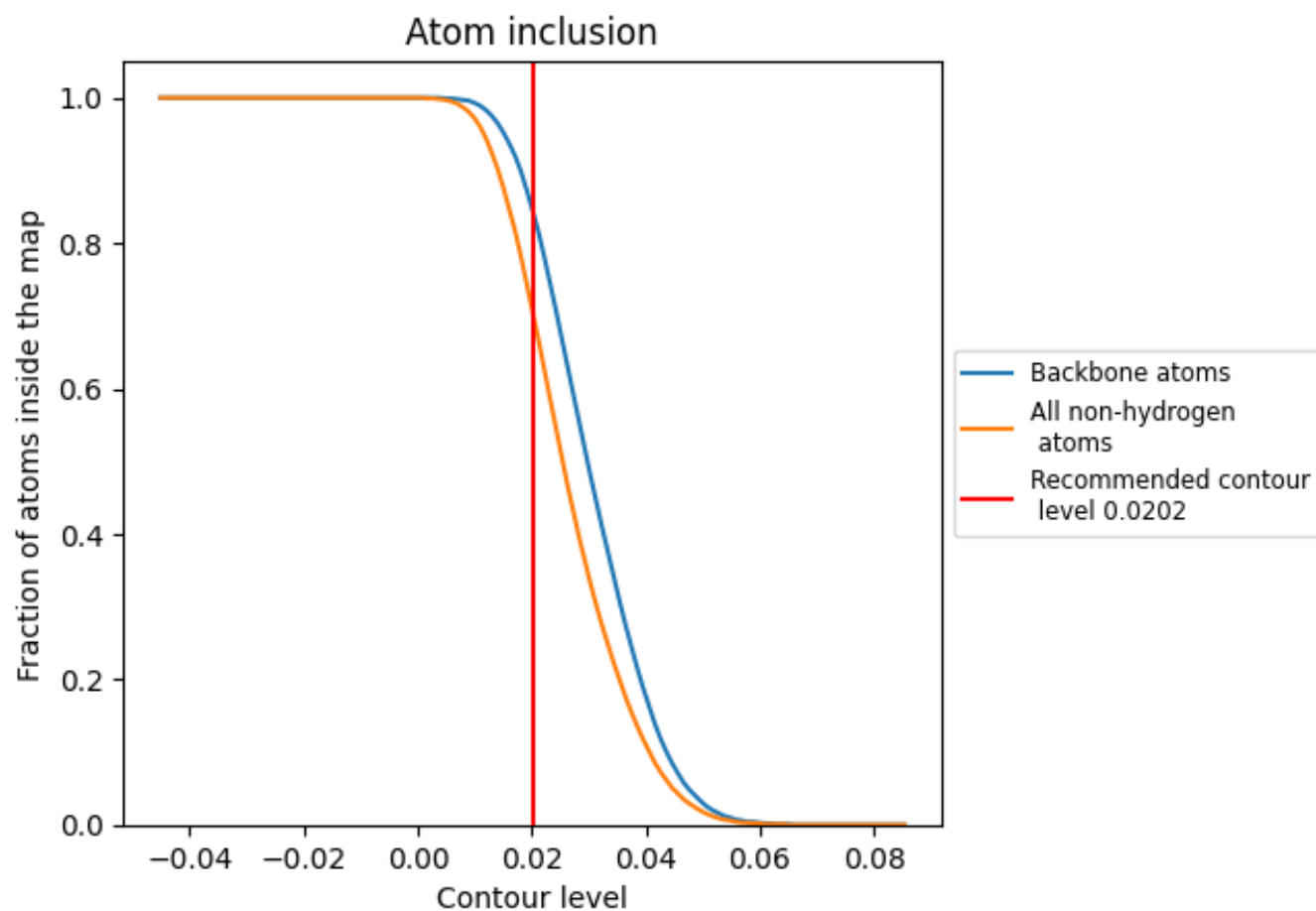
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

9.3 Atom inclusion mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.0202).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 84% of all backbone atoms, 70% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ





















































































The table lists the average atom inclusion at the recommended contour level (0.0202) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7050	 0.3990
0	 0.7160	 0.3720
1	 0.7220	 0.3650
2	 0.6030	 0.4280
3	 0.6310	 0.4510
4	 0.6170	 0.4520
5	 0.5960	 0.4400
6	 0.6170	 0.4380
7	 0.6030	 0.4310
8	 0.7980	 0.4280
9	 0.7900	 0.4180
A	 0.7950	 0.4600
AA	 0.7940	 0.4330
AB	 0.5870	 0.3620
AC	 0.5720	 0.3570
AD	 0.6160	 0.3600
AE	 0.5720	 0.3630
AF	 0.5730	 0.3600
AG	 0.5900	 0.3610
AH	 0.5680	 0.3620
AI	 0.5750	 0.3620
AJ	 0.5970	 0.3610
AK	 0.5830	 0.3580
AL	 0.5790	 0.3620
AM	 0.6130	 0.3570
AN	 0.5680	 0.3610
AO	 0.5740	 0.3610
AP	 0.5930	 0.3610
AQ	 0.5920	 0.3780
AR	 0.5910	 0.3690
AS	 0.6200	 0.3640
B	 0.7630	 0.4530
C	 0.8000	 0.4570
D	 0.7920	 0.4600
E	 0.7650	 0.4520













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Chain	Atom inclusion	Q-score
F	 0.7640	 0.4510
G	 0.8130	 0.4750
H	 0.8400	 0.4850
I	 0.8510	 0.4550
J	 0.8300	 0.4530
K	 0.7900	 0.4450
L	 0.7190	 0.3750
M	 0.7950	 0.4130
N	 0.7990	 0.4160
O	 0.6760	 0.3500
P	 0.8420	 0.4440
Q	 0.8210	 0.4700
R	 0.8200	 0.4810
S	 0.8370	 0.4630
T	 0.8310	 0.4520
U	 0.8210	 0.4580
V	 0.7150	 0.3730
W	 0.8000	 0.4130
X	 0.7950	 0.4180
Y	 0.7130	 0.3630
Z	 0.8470	 0.4440
a	 0.8040	 0.4700
b	 0.8440	 0.4860
c	 0.8430	 0.4560
d	 0.8330	 0.4520
e	 0.8230	 0.4560
f	 0.7250	 0.3750
g	 0.7970	 0.4100
h	 0.7970	 0.4150
i	 0.6680	 0.3500
j	 0.8460	 0.4470
k	 0.8160	 0.4710
l	 0.8290	 0.4850
m	 0.8350	 0.4620
n	 0.7830	 0.4470
o	 0.7140	 0.3710
p	 0.7200	 0.3670
q	 0.8050	 0.4750
r	 0.8370	 0.4870
s	 0.8450	 0.4530
t	 0.8210	 0.4560
u	 0.7280	 0.3760

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Chain	Atom inclusion	Q-score
v	 0.6760	 0.3520
w	 0.8170	 0.4690
x	 0.8270	 0.4840
y	 0.8320	 0.4630
z	 0.7930	 0.4490